
WATERMAN

(TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Wed Aug 16 09:56:08 2000; MasPar time 12.82 Seconds
Molecular output not generated. 546.075 Million cell updates/sec

Title: >US-09-427-873-2
Description: (1-101) from US09427873.pep
Perfect Score: 101
Sequence: 1 LGKFSQTCYNALQGSVLTS.....STKINLDDHIANIDGTLKYE 101

Scoring table: TABLE unitprotatable
Gap 60

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database: sptrembl12
1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human
5:sp.invertebrate 6:sp.mammal 7:sp.mhc 8:sp.organelle
9:sp.phage 10:sp.plant 11:sp.rodent 12:sp.unclassified
13:sp.vertebrate 14:sp.virus

Statistics: Mean 3.138; Variance 0.377; scale 8.331

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred No.
1	8	7.9	994	5	DORSAL B.	1.18e-03
2	7	6.9	100	2	HYPOTHETICAL PROTEIN (1.86e-01
3	7	6.9	241	2	MOLYBDENUM-BINDING SUB	1.86e-01
4	7	6.9	261	2	HYPOTHETICAL 26.5 KD P	1.86e-01
5	7	6.9	263	5	COSMID F58CA	1.86e-01
6	7	6.9	285	10	RIBOSOME-INACTIVATING	1.86e-01
7	7	6.9	399	10	LOW AFFINITY CALCIUM A	1.86e-01
8	7	6.9	402	2	POLYNUCLEOTIDE ADENYL	1.86e-01
9	7	6.9	440	2	ADENYLOSUCCINATE LYASE	1.86e-01
10	7	6.9	465	14	ORF MSV179 PUTATIVE ME	1.86e-01
11	7	6.9	606	2	ENDO-BETA-1,4-XYLANASE	1.86e-01
12	7	6.9	938	10	F20N2.12.	1.86e-01
13	7	6.9	1115	11	PER3 (FRAGMENT).	1.86e-01
14	7	6.9	1152	4	KIAA0204 PROTEIN.	1.86e-01
15	7	6.9	1204	4	HSK.	1.86e-01
16	6	5.9	61	2	L0012.	1.80e+01
17	6	5.9	85	14	ACMNPV ORF76.	1.80e+01
18	6	5.9	91	14	FRAGMENT OF 28K VIRULE	1.80e+01
19	6	5.9	92	10	PHOSPHOENOLPYRUVATE CA	1.80e+01
20	6	5.9	94	2	UNCERTAIN (FRAGMENT).	1.80e+01

PUTATIVE GLUTAREDOXIN. 1.80e+01
109AA LONG HYPOTHETICAL 1.80e+01
BILF2-PUTATIVE GLYCOPR 1.80e+01
COSMID T14B4. 1.80e+01
COLIA1 AND PDGFB FUSIO 1.80e+01
ATAF1-LIKE PROTEIN (FR 1.80e+01
PDGF B (FRAGMENT). 1.80e+01
HYPOTHETICAL 17.8 KD P 1.80e+01
HYPOTHETICAL 17.8 KD P 1.80e+01
GUANINE NUCLEOTIDE EXC 1.80e+01
ARP-LIKE PROTEIN. 1.80e+01
CLONE B2-24B HOMOLOG O 1.80e+01
HYPOTHETICAL 20.6 KD P 1.80e+01
PTS SYSTEM, NITROGEN R 1.80e+01
C-SIS PROTO-ONCOGENE (1.80e+01
FUCULOSE-1-PHOSPHATE A 1.80e+01
VIF PROTEIN. 1.80e+01
VIF PROTEIN. 1.80e+01
W04D2.5 PROTEIN. 1.80e+01
C-SIS ONCOGENE (PLATEL 1.80e+01
F28C6.5 PROTEIN. 1.80e+01
VDEJ PROTEIN. 1.80e+01
V-SIS TRANSFORMING PRO 1.80e+01
CODED FOR BY C. ELEGAN 1.80e+01
HYPOTHETICAL 25.6 KD P 1.80e+01
ALEURONE RIBONUCLEASE 1.80e+01
RING ZINC FINGER-CONTA 1.80e+01
41KB FRAGMENT FROM LE 1.80e+01
ANTI REPRESSOR. 1.80e+01
TONOPLAST INTRINSIC PR 1.80e+01
SEC22 HOMOLOG. 1.80e+01
DIVERGED SERINE PROTEA 1.80e+01
ACCESSORY GLAND-SPECIF 1.80e+01
SIGF. 1.80e+01
STRESS RESPONSE/STATIO 1.80e+01
3-METHYL-2-OXOBUTANOA 1.80e+01
N-ACETYL-MANNOSAMINE TR 1.80e+01
PHA DEPOLYMERASE PRECU 1.80e+01
ATAF1-LIKE PROTEIN (FR 1.80e+01
SEC22 HOMOLOG. 1.80e+01
HEAT SHOCK TRANSCRIPTI 1.80e+01
HEAT SHOCK TRANSCRIPTI 1.80e+01
HYPOTHETICAL 31.5 KD P 1.80e+01
HYPOTHETICAL 32.8 KD P 1.80e+01
MC084L. 1.80e+01
EC70-ATP DIPHOSPHOHYD 1.80e+01
G2-LIKE. 1.80e+01
HYPOTHETICAL 35.2 KD P 1.80e+01
PROTODHERIN 5 (FRAGM 1.80e+01
HYPOTHETICAL 35.4 KD P 1.80e+01
GAG-RELATED PROTEIN (F 1.80e+01
NITROGENASE REDUCTASE. 1.80e+01
PLASMID RECOMBINATION. 1.80e+01
REVERSE TRANSCRIPTASE 1.80e+01
VP7. 1.80e+01
ZINC FINGER PROTEIN. 1.80e+01
OUTER MEMBRANE PROTEIN 1.80e+01
T10C6.7 PROTEIN. 1.80e+01
ISOLQUIRITIGENIN 2'-O 1.80e+01
DELTA 12 FATTY ACID EP 1.80e+01
POLY(A) POLYMERASE (EC 1.80e+01
PERITROPHIN-48A PRECUR 1.80e+01
MYOSIN HEAVY CHAIN B (1.80e+01
DELTA-12 FATTY ACID DE 1.80e+01
ATMB1 PROTEIN. 1.80e+01
42 KD PROTEIN. 1.80e+01
POLY(A) POLYMERASE. 1.80e+01
C08H9.6 PROTEIN. 1.80e+01
RIBULOSE BISPHOSPHATE 1.80e+01
GLUTAMATE SYMPORT. 1.80e+01
CD44 ANTIGEN (HOMING R 1.80e+01
CD44 ANTIGEN (CD44) (F 1.80e+01
F8K4.20 PROTEIN. 1.80e+01

94	6	5.9	418	4	075066	KIAA0478 PROTEIN.	1.80e+01	167	6	5.9	838	10	049372	HYPOHETICAL 92.4 KD P	1.80e+01
95	6	5.9	420	14	067008	POLYPYRROLINE PRECURSOR	1.80e+01	168	6	5.9	857	14	073289	ENVELOPE GLYCOPROTEIN.	1.80e+01
96	6	5.9	420	2	085656	SERINE HYDROXYMETHYLTR	1.80e+01	169	6	5.9	869	4	000513	GUANINE NUCLEOTIDE EXC	1.80e+01
97	6	5.9	426	2	053615	SERINE HYDROXYMETHYLTR	1.80e+01	170	6	5.9	878	4	09Y5C2	PROTODADHERIN GAMMA C5	1.80e+01
98	6	5.9	426	2	053441	SERINE HYDROXYMETHYLTR	1.80e+01	171	6	5.9	879	5	09XZ14	HYPOHETICAL 100.1 KD	1.80e+01
99	6	5.9	436	2	09Y794	PUTATIVE SERINE HYDROX	1.80e+01	172	6	5.9	882	5	021567	M28-4 PROTEIN.	1.80e+01
100	6	5.9	434	2	052963	CHEMOTAXIS MOTIC PROTEI	1.80e+01	173	6	5.9	900	14	012936	PUTATIVE DNA-DIRECTED	1.80e+01
101	6	5.9	434	2	054327	TOXIN DEGRADING PROTEA	1.80e+01	174	6	5.9	912	4	092888	GUANINE NUCLEOTIDE EXC	1.80e+01
102	6	5.9	437	11	035249	CD44 (FRAGMENT).	1.80e+01	175	6	5.9	919	11	092116	LSC PROTEIN.	1.80e+01
103	6	5.9	440	2	007120	SURFACE LAYER PROTEIN.	1.80e+01	176	6	5.9	919	11	061210	LYMPHOID BLAST CRISIS	1.80e+01
104	6	5.9	445	5	09YXW4	COP9 COMPLEX HOMOLOG S	1.80e+01	177	6	5.9	944	4	09Y5F6	PROTODADHERIN GAMMA C5	1.80e+01
105	6	5.9	446	1	029791	PHOSPHOMANNOMUTASE (PM	1.80e+01	178	6	5.9	967	5	018281	SIMILARITY TO VERY-LON	1.80e+01
106	6	5.9	448	2	034824	YBBT PROTEIN.	1.80e+01	179	6	5.9	968	10	081357	PHOSPHENOLPYRUVATE CA	1.80e+01
107	6	5.9	448	2	087090	YBBT PROTEIN.	1.80e+01	180	6	5.9	1007	11	062641	GLUTAMATE RECEPTOR DEL	1.80e+01
108	6	5.9	455	8	003658	RIBULOSE BISPHOSPHATE	1.80e+01	181	6	5.9	1007	11	062641	GLUTAMATE RECEPTOR CHA	1.80e+01
109	6	5.9	456	2	048508	SB-PROTEIN PRECURSOR.	1.80e+01	182	6	5.9	1007	11	062641	GLUTAMATE RECEPTOR DEL	1.80e+01
110	6	5.9	457	10	080701	F8K4.15 PROTEIN.	1.80e+01	183	6	5.9	1007	4	043424	GLUTAMATE RECEPTOR SUB	1.80e+01
111	6	5.9	460	14	09NSO6	HYPOHETICAL 51.1 KD P	1.80e+01	184	6	5.9	1008	11	062226	GLUTAMATE RECEPTOR SUB	1.80e+01
112	6	5.9	466	8	098743	RIBULOSE BISPHOSPHATE	1.80e+01	185	6	5.9	1008	11	0921X1	GLUT4 VESICLE PROTEIN.	1.80e+01
113	6	5.9	475	8	09XOC1	RIBULOSE BISPHOSPHATE	1.80e+01	186	6	5.9	1009	5	090731	B0365.1 PROTEIN.	1.80e+01
114	6	5.9	475	8	09XOC2	RIBULOSE BISPHOSPHATE	1.80e+01	187	6	5.9	1149	10	082331	PUTATIVE REVERSE TRANS	1.80e+01
115	6	5.9	475	8	092255	RIBULOSE BISPHOSPHATE	1.80e+01	188	6	5.9	1192	5	046072	COSMID 30B8.	1.80e+01
116	6	5.9	476	8	092255	CYTCHROME C OXIDASE S	1.80e+01	189	6	5.9	1201	5	024240	ACTIN BINDING PROTEIN.	1.80e+01
117	6	5.9	476	8	092252	CYTCHROME C OXIDASE S	1.80e+01	190	6	5.9	1231	11	055092	SERINE/THREONINE KINASE	1.80e+01
118	6	5.9	477	8	062944	RIBULOSE BISPHOSPHATE	1.80e+01	191	6	5.9	1262	3	013327	PROTEIN PHOSPHATASE SS	1.80e+01
119	6	5.9	477	5	026218	CYTCHROME C OXIDASE S	1.80e+01	192	6	5.9	1413	10	092VW0	PUTATIVE RETROTRANSPOS	1.80e+01
120	6	5.9	478	8	063176	CYTCHROME C OXIDASE S	1.80e+01	193	6	5.9	1426	3	078577	ATP-BINDING CASSETTE M	1.80e+01
121	6	5.9	483	14	09NAU1	HEXON PROTEIN (FRAGMEN	1.80e+01	194	6	5.9	1490	5	001319	F02E9.4 PROTEIN.	1.80e+01
122	6	5.9	485	2	09WXP2	HYPOHETICAL 55.6 KD P	1.80e+01	195	6	5.9	1503	10	081283	T14F8.24 PROTEIN.	1.80e+01
123	6	5.9	490	2	085997	SEMIALDEHYDE DEHYDROGE	1.80e+01	196	6	5.9	1522	4	015085	KIAA0380.	1.80e+01
124	6	5.9	504	14	074117	GP105 (FRAGMENT).	1.80e+01	197	6	5.9	1539	4	015078	KIAA0373.	1.80e+01
125	6	5.9	507	14	074115	GP105 (FRAGMENT).	1.80e+01	198	6	5.9	1676	10	023332	CENTROMERE PROTEIN HOM	1.80e+01
126	6	5.9	508	14	074118	GP105 (FRAGMENT).	1.80e+01	199	6	5.9	1679	5	026607	SURFACE PROTEIN (FRAGM	1.80e+01
127	6	5.9	508	14	074116	GP105 (FRAGMENT).	1.80e+01	200	6	5.9	1732	10	023576	DNA CHROMOSOME 4, ESSA	1.80e+01
128	6	5.9	512	2	008251	LIPOPROTEIN.	1.80e+01	201	6	5.9	1829	4	015015	KIAA0296.	1.80e+01
129	6	5.9	519	5	046018	ZK570.1 PROTEIN.	1.80e+01	202	6	5.9	1890	10	049528	GENE 11-1 PROTEIN - LI	1.80e+01
130	6	5.9	549	4	099475	KM-102-DERIVED REDUCTA	1.80e+01	203	6	5.9	1992	13	040834	NONMUSCLE MYOSIN HEAVY	1.80e+01
131	6	5.9	551	2	071732	HYPOHETICAL 61.4 KD P	1.80e+01	204	6	5.9	2030	5	061850	F55F10.2 PROTEIN.	1.80e+01
132	6	5.9	559	5	077472	LEUCINE-RICH REPEAT PR	1.80e+01	205	6	5.9	2160	5	017709	H05L14.2 PROTEIN.	1.80e+01
133	6	5.9	561	2	033131	HYPOHETICAL 61.8 KD P	1.80e+01	206	6	5.9	2253	4	095850	POLYCYSTIC KIDNEY DISE	1.80e+01
134	6	5.9	565	2	051685	HYPOHETICAL 65.7 KD P	1.80e+01	207	6	5.9	2610	5	019482	F15B9.7 PROTEIN.	1.80e+01
135	6	5.9	568	2	0929G0	PREDICTED OMP.	1.80e+01	208	6	5.9	3512	5	062524	CPY GENE.	1.80e+01
136	6	5.9	568	3	0927M1	PUTATIVE OXALYL-COA DE	1.80e+01	209	6	5.9	3726	5	027255	TRITHORAX PROTEIN TRX.	1.80e+01
137	6	5.9	569	10	084506	T20P6.9 PROTEIN.	1.80e+01	210	6	5.9	3828	5	024742	PREDICTED TRITHORAX PR	1.80e+01
138	6	5.9	572	5	022875	AC7.2 PROTEIN.	1.80e+01	211	5	5.0	37	14	090372	HAEMAGGLUTININ-NEURAM	1.80e+02
139	6	5.9	577	5	024571	SOB PROTEIN.	1.80e+01	212	5	5.0	40	14	068321	E2/NS1 (FRAGMENT).	9.24e+02
140	6	5.9	582	10	09XIW5	SIMILAR TO GLYCINE MAX	1.80e+01	213	5	5.0	43	14	09YPD3	ENVELOPE PROTEIN (FRAG	9.24e+02
141	6	5.9	586	3	094019	TRANSPORT PROTEIN.	1.80e+01	214	5	5.0	46	14	079935	POL (FRAGMENT).	9.24e+02
142	6	5.9	586	9	084308	REPLICASE.	1.80e+01	215	5	5.0	46	14	082279	REVERSE TRANSCRIPTASE	9.24e+02
143	6	5.9	599	10	080528	FLA309.11 PROTEIN.	1.80e+01	216	5	5.0	46	14	082287	REVERSE TRANSCRIPTASE	9.24e+02
144	6	5.9	624	2	095626	METHYLATION ACCEPTING	1.80e+01	217	5	5.0	46	14	079934	POL (FRAGMENT).	9.24e+02
145	6	5.9	637	5	093512	F15D4.4 PROTEIN.	1.80e+01	218	5	5.0	46	14	079941	POL (FRAGMENT).	9.24e+02
146	6	5.9	638	1	026315	FEROUS IRON TRANSPORT	1.80e+01	219	5	5.0	46	14	079940	POL (FRAGMENT).	9.24e+02
147	6	5.9	640	5	09XWZ6	Y42A5A.2 PROTEIN.	1.80e+01	220	5	5.0	46	14	079940	POL (FRAGMENT).	9.24e+02
148	6	5.9	643	5	022886	SIMILARITY TO EGF-LIKE	1.80e+01	221	5	5.0	46	14	055266	POL POLYPROTEIN (FRAGM	9.24e+02
149	6	5.9	674	11	093772	GROWTH POTENTIATING FA	1.80e+01	222	5	5.0	49	14	09W9S5	POLYPROTEIN (FRAGMENT)	9.24e+02
150	6	5.9	676	5	045553	F53A2.8 PROTEIN (EC 3.	1.80e+01	223	5	5.0	70	14	087344	ENVELOPE GLYCOPROTEIN	9.24e+02
151	6	5.9	697	4	043167	KIAA0441.	1.80e+01	224	5	5.0	70	14	087341	ENVELOPE GLYCOPROTEIN	9.24e+02
152	6	5.9	700	2	072127	FLAGELLIN (FRAGMENT).	1.80e+01	225	5	5.0	72	14	09YRD0	FUSION PROTEIN (FRAGME	9.24e+02
153	6	5.9	701	11	0921X5	GLUT4 VESICLE PROTEIN.	1.80e+01	226	5	5.0	72	14	087436	ENVELOPE GLYCOPROTEIN	9.24e+02
154	6	5.9	708	5	091954	ACETYLCHOLINESTERASE.	1.80e+01	227	5	5.0	73	14	087433	ENVELOPE GLYCOPROTEIN	9.24e+02
155	6	5.9	712	4	091557	DJ1163J1.3 (NOVEL PROT	1.80e+01	228	5	5.0	76	13	090641	CAMP-DEPENDENT PROTEIN	9.24e+02
156	6	5.9	720	1	073955	HYDROPEROXIDASE.	1.80e+01	229	5	5.0	84	14	036993	FUSION PROTEIN (FRAGME	9.24e+02
157	6	5.9	765	2	092LEB	PUTATIVE HYDANTOIN UTI	1.80e+01	230	5	5.0	84	14	036999	FUSION PROTEIN (FRAGME	9.24e+02
158	6	5.9	765	2	025403	N-METHYLHYDANTOINASE.	1.80e+01	231	5	5.0	89	5	096919	TC1-LIKE TRANSPOSASE (9.24e+02
159	6	5.9	775	4	060347	KIAA0608 PROTEIN (FRAG	1.80e+01	232	5	5.0	90	2	024880	HYPOHETICAL 10.2 KD P	9.24e+02
160	6	5.9	780	11	008779	CD44 PROTEIN.	1.80e+01	233	5	5.0	92	10	092TM9	PGP219.	9.24e+02
161	6	5.9	780	4	075157	KIAA0669 PROTEIN.	1.80e+01	234	5	5.0	93	13	013002	ZP3 HOMOLOG (FRAGMENT)	9.24e+02
162	6	5.9	808	10	092R56	RIBONUCLEOTIDE REDUCTA	1.80e+01	235	5	5.0	94	11	062507	COCHLEAR MRNA (CLONE 3	9.24e+02
163	6	5.9	808	10	092R57	RIBONUCLEOTIDE REDUCTA	1.80e+01	236	5	5.0	98	2	092J78	PUTATIVE.	9.24e+02
164	6	5.9	809	3	086693	CHROMOSOME XV READING	1.80e+01	237	5	5.0	98	2	025941	HYPOHETICAL 11.0 KD P	9.24e+02
165	6	5.9	810	3	002553	P53 ACTIVITY REGULATOR	1.80e+01	238	5	5.0	107	3	005413	DNA FOR ORF'S FROM CHR	9.24e+02
166	6	5.9	827	10	004578	SEQUENCE OF BAC F19K23	1.80e+01	239	5	5.0	109	8	047626	CYTCHROME B (FRAGMENT	9.24e+02
											110	10	023624	FPP1 PROTEIN.	9.24e+02

240	5	5.0	110	2	Q92863	HIT FAMILY HYDROLASE.	9.24e+02	313	5	5.0	212	2	Q25248	CONSERVED HYPOTHETICAL	9.24e+02
241	5	5.0	111	8	Q47623	CYTOCHROME B (FRAGMENT	9.24e+02	314	5	5.0	214	13	Q62134	'DNA TOPOISOMERASE IIB	9.24e+02
242	5	5.0	115	10	Q23759	UBIQUITIN PROTEIN.	9.24e+02	315	5	5.0	214	11	Q63177	P103.	9.24e+02
243	5	5.0	116	14	Q82356	HTLV-II PROVIRUS POL G	9.24e+02	316	5	5.0	215	2	Q50970	P103.	9.24e+02
244	5	5.0	116	14	Q82342	HTLV-II PROVIRUS POL G	9.24e+02	317	5	5.0	216	5	Q01253	T2003.1 PROTEIN.	9.24e+02
245	5	5.0	118	11	Q95301	INTERPHOTORECEPTOR RET	9.24e+02	318	5	5.0	218	14	Q93774	MA56 PRECURSOR.	9.24e+02
246	5	5.0	119	5	Q17424	PROBABLE THIOREDOLIN.	9.24e+02	319	5	5.0	220	3	Q05778	CHROMOSOME XII COSMID	9.24e+02
247	5	5.0	123	14	Q9A25	POLYPROTEIN (FRAGMENT)	9.24e+02	320	5	5.0	220	3	Q9AXH8	OMPA.	9.24e+02
248	5	5.0	123	14	Q9A25	POLYPROTEIN (FRAGMENT)	9.24e+02	321	5	5.0	220	2	Q45415	VSRC.	9.24e+02
249	5	5.0	127	6	Q40209	THYROGLOBULIN (FRAGMENT)	9.24e+02	322	5	5.0	221	3	Q04178	D9509.18P.	9.24e+02
250	5	5.0	128	8	Q35285	CYTOCHROME OXIDASE I (9.24e+02	323	5	5.0	221	8	Q36717	LIGHT-HARVESTING COMPL	9.24e+02
251	5	5.0	129	1	Q9YF58	129AA LONG HYPOTHETICA	9.24e+02	324	5	5.0	228	1	Q59035	228AA LONG HYPOTHETICA	9.24e+02
252	5	5.0	129	2	P73361	HYPOTHETICAL 14.9 KD P	9.24e+02	325	5	5.0	230	10	Q9XIV0	MRNA EXPRESSED IN CUCU	9.24e+02
253	5	5.0	130	5	Q9XV43	F36D1.7 PROTEIN.	9.24e+02	326	5	5.0	230	2	Q59521	HYPOTHETICAL 24.5 KD P	9.24e+02
254	5	5.0	130	14	Q55668	FUSION PROTEIN (FRAGME	9.24e+02	327	5	5.0	231	1	Q58733	HYPOTHETICAL PROTEIN M	9.24e+02
255	5	5.0	130	14	Q55666	FUSION PROTEIN (FRAGME	9.24e+02	328	5	5.0	231	2	Q58733	F35B12.3 PROTEIN.	9.24e+02
256	5	5.0	130	14	Q55674	FUSION PROTEIN (FRAGME	9.24e+02	329	5	5.0	232	10	Q65705	HYPOTHETICAL 26.4 KD P	9.24e+02
257	5	5.0	130	14	Q55674	FUSION PROTEIN (FRAGME	9.24e+02	330	5	5.0	233	13	Q42185	CARAMOYL-PHOSPHATE SY	9.24e+02
258	5	5.0	130	14	Q55672	FUSION PROTEIN (FRAGME	9.24e+02	331	5	5.0	235	1	Q73952	BIOTIN LIGASE BIRA HOM	9.24e+02
259	5	5.0	130	14	Q55681	FUSION PROTEIN (FRAGME	9.24e+02	332	5	5.0	235	11	Q63471	PAROTID SECRETORY PROT	9.24e+02
260	5	5.0	132	9	Q9XJP0	P12 (FRAGMENT).	9.24e+02	333	5	5.0	236	2	Q84313	HYPOTHETICAL 26.3 KD P	9.24e+02
261	5	5.0	134	14	Q39518	RNA DEPENDENT RNA POLY	9.24e+02	334	5	5.0	238	14	Q9WHX7	MATRIX PROTEIN M1 (FRA	9.24e+02
262	5	5.0	135	10	Q64622	F19F24.12 PROTEIN.	9.24e+02	335	5	5.0	238	2	Q54417	MALONATE DECARBOXYLASE	9.24e+02
263	5	5.0	138	13	Q9XGQ9	CADHERIN (FRAGMENT).	9.24e+02	336	5	5.0	238	11	Q08627	PROLACTIN-LIKE PROTEIN	9.24e+02
264	5	5.0	140	14	Q9WF47	FUSION GLYCOPROTEIN PR	9.24e+02	337	5	5.0	239	14	Q9WHX8	MATRIX PROTEIN M1 (FRA	9.24e+02
265	5	5.0	141	2	Q56934	FUSION GLYCOPROTEIN PR	9.24e+02	338	5	5.0	239	14	Q9WHY0	MATRIX PROTEIN M1 (FRA	9.24e+02
266	5	5.0	141	2	Q56934	SYCH.	9.24e+02	339	5	5.0	239	14	Q9WHY1	MATRIX PROTEIN M1 (FRA	9.24e+02
267	5	5.0	142	14	Q9WF45	FUSION GLYCOPROTEIN PR	9.24e+02	340	5	5.0	239	14	Q9WHX9	MATRIX PROTEIN M1 (FRA	9.24e+02
268	5	5.0	142	3	Q92425	MANGANESE-SUPEROXIDE D	9.24e+02	341	5	5.0	239	14	Q9WHY7	MATRIX PROTEIN M1 (FRA	9.24e+02
269	5	5.0	142	3	Q92424	MANGANESE-SUPEROXIDE D	9.24e+02	342	5	5.0	239	14	Q9WHY6	MATRIX PROTEIN M1 (FRA	9.24e+02
270	5	5.0	144	14	Q9WGF0	FUSION GLYCOPROTEIN PR	9.24e+02	343	5	5.0	239	14	Q9WHY9	MATRIX PROTEIN M1 (FRA	9.24e+02
271	5	5.0	144	14	Q9WGF9	MAJOR CAPSID PROTEIN L	9.24e+02	344	5	5.0	239	14	Q9WHY8	MATRIX PROTEIN M1 (FRA	9.24e+02
272	5	5.0	145	10	Q40431	PSI-H PRECURSOR.	9.24e+02	345	5	5.0	239	14	Q9WHY3	MATRIX PROTEIN M1 (FRA	9.24e+02
273	5	5.0	146	14	Q9WGF4	MAJOR CAPSID PROTEIN L	9.24e+02	346	5	5.0	239	14	Q9WHY4	MATRIX PROTEIN M1 (FRA	9.24e+02
274	5	5.0	149	10	Q65857	GLUTATHIONE S-TRANSFER	9.24e+02	347	5	5.0	241	2	Q67285	ALCOHOL DEHYDROGENASE	9.24e+02
275	5	5.0	150	14	Q9WF37	FUSION GLYCOPROTEIN PR	9.24e+02	348	5	5.0	241	2	Q67285	POLYHEDRIN.	9.24e+02
276	5	5.0	151	14	Q9WF33	FUSION GLYCOPROTEIN PR	9.24e+02	349	5	5.0	245	14	Q9YMX2	WATER CHANNEL PROTEIN	9.24e+02
277	5	5.0	151	14	Q9WF41	FUSION GLYCOPROTEIN PR	9.24e+02	350	5	5.0	245	14	Q9YMX2	14-3-3 PROTEIN	9.24e+02
278	5	5.0	151	14	Q9WF38	FUSION GLYCOPROTEIN PR	9.24e+02	351	5	5.0	248	10	Q9XF76	14-3-3 PROTEIN	9.24e+02
279	5	5.0	151	7	Q98204	MHC CLASS I (FRAGMENT)	9.24e+02	352	5	5.0	249	10	P93787	MATRIX PROTEIN M1 (FRA	9.24e+02
280	5	5.0	153	14	Q9WF42	FUSION GLYCOPROTEIN PR	9.24e+02	353	5	5.0	250	14	Q9WHY2	MATRIX PROTEIN M1.	9.24e+02
281	5	5.0	154	14	Q9WF39	FUSION GLYCOPROTEIN PR	9.24e+02	354	5	5.0	252	14	Q9W9L6	MATRIX PROTEIN M1.	9.24e+02
282	5	5.0	154	14	Q9YF57	FUSION GLYCOPROTEIN PR	9.24e+02	355	5	5.0	252	14	Q98711	MATRIX PROTEIN.	9.24e+02
283	5	5.0	154	14	Q84411	GENOME, PARTIAL SEQUE	9.24e+02	356	5	5.0	252	14	Q9W8D8	MATRIX PROTEIN 1.	9.24e+02
284	5	5.0	154	14	Q97659	ENVELOPE GLYCOPROTEIN	9.24e+02	357	5	5.0	252	14	Q9WB24	MATRIX PROTEIN 1.	9.24e+02
285	5	5.0	157	10	Q39338	OLEOSIN.	9.24e+02	358	5	5.0	252	14	Q9WB24	MATRIX PROTEIN 1.	9.24e+02
286	5	5.0	164	5	Q01778	CODED FOR BY C. ELEGAN	9.24e+02	359	5	5.0	252	14	Q9WB26	MATRIX PROTEIN 1.	9.24e+02
287	5	5.0	164	10	Q38835	HYPOTHETICAL 17.7 KD P	9.24e+02	360	5	5.0	252	14	Q9WC01	MATRIX PROTEIN 1.	9.24e+02
288	5	5.0	165	7	Q98207	MHC CLASS I (FRAGMENT)	9.24e+02	361	5	5.0	252	14	Q9WB29	MATRIX PROTEIN 1.	9.24e+02
289	5	5.0	169	2	Q92C79	102 KBASES UNSTABLE RE	9.24e+02	362	5	5.0	252	14	Q9WB29	MATRIX PROTEIN 1.	9.24e+02
290	5	5.0	170	7	Q98210	MHC CLASS I (FRAGMENT)	9.24e+02	363	5	5.0	252	14	Q9WB34	MATRIX PROTEIN 1.	9.24e+02
291	5	5.0	171	1	Q27890	CONSERVED PROTEIN.	9.24e+02	364	5	5.0	252	14	Q9WB34	MATRIX PROTEIN 1.	9.24e+02
292	5	5.0	173	10	Q22257	HYPOTHETICAL PROTEIN.	9.24e+02	365	5	5.0	252	14	Q9WC04	MATRIX PROTEIN 1.	9.24e+02
293	5	5.0	176	14	Q9YFHI	TRIPLE-GENE-BLOCK THIR	9.24e+02	366	5	5.0	252	14	Q9WC06	MATRIX PROTEIN 1.	9.24e+02
294	5	5.0	180	5	Q18997	D2089.2 PROTEIN.	9.24e+02	367	5	5.0	252	14	Q9WB30	MATRIX PROTEIN 1.	9.24e+02
295	5	5.0	181	2	Q68404	ALPHA HEMOLYSIN (FRAGM	9.24e+02	368	5	5.0	252	14	Q9WB30	MATRIX PROTEIN 1.	9.24e+02
296	5	5.0	181	2	Q70070	ALPHA HEMOLYSIN (FRAGM	9.24e+02	369	5	5.0	252	14	Q9WB22	MATRIX PROTEIN 1.	9.24e+02
297	5	5.0	182	3	Q93973	ALLERGEN (FRAGMENT).	9.24e+02	370	5	5.0	252	14	Q9WB22	MATRIX PROTEIN 1.	9.24e+02
298	5	5.0	183	10	Q64933	MADS BOX PROTEIN.	9.24e+02	371	5	5.0	252	14	Q9WB22	MATRIX PROTEIN M1.	9.24e+02
299	5	5.0	189	14	P90446	VIRION PROTEIN.	9.24e+02	372	5	5.0	252	14	Q9YIL2	M1 PROTEIN.	9.24e+02
300	5	5.0	189	14	P90446	VIRION PROTEIN.	9.24e+02	373	5	5.0	252	14	Q9YF63	M1 PROTEIN.	9.24e+02
301	5	5.0	193	5	Q76215	DENSE GRANULE PROTEIN	9.24e+02	374	5	5.0	252	14	Q89562	MEMBRANE PROTEIN M1.	9.24e+02
302	5	5.0	194	2	Q69747	IGAL PROTEASE (FRAGMEN	9.24e+02	375	5	5.0	252	14	Q67157	MEMBRANE PROTEIN M1.	9.24e+02
303	5	5.0	195	14	P89530	PUTATIVE COAT PROTEIN	9.24e+02	376	5	5.0	252	14	Q67152	MATRIX PROTEIN.	9.24e+02
304	5	5.0	200	2	Q9X6E9	PHENYLALANYL-TRNA-SYNT	9.24e+02	377	5	5.0	252	14	Q67161	MEMBRANE PROTEIN M1.	9.24e+02
305	5	5.0	202	14	Q95833	COAT PROTEIN.	9.24e+02	378	5	5.0	252	14	Q67147	MATRIX PROTEIN 1.	9.24e+02
306	5	5.0	202	14	Q65834	COAT PROTEIN.	9.24e+02	379	5	5.0	253	10	Q9ZST8	TIC20.	9.24e+02
307	5	5.0	202	14	Q65840	COAT PROTEIN.	9.24e+02	380	5	5.0	254	5	Q62154	F11d11.5 PROTEIN.	9.24e+02
308	5	5.0	202	14	Q65839	COAT PROTEIN.	9.24e+02	381	5	5.0	256	14	Q9NM14	FUSION PROTEIN (FRAGME	9.24e+02
309	5	5.0	202	14	Q65841	COAT PROTEIN.	9.24e+02	382	5	5.0	256	14	Q9NM12	FUSION PROTEIN (FRAGME	9.24e+02
310	5	5.0	202	14	Q65842	COAT PROTEIN.	9.24e+02	383	5	5.0	259	5	Q18600	DVTRY-2 TRYPSIN PRECUS	9.24e+02
311	5	5.0	202	2	Q9WYA6	HYPOTHETICAL 22.9 KD P	9.24e+02	384	5	5.0	259	2	Q87819	OTSB PROTEIN.	9.24e+02
312	5	5.0	206	3	Q06346	CHROMOSOME IV COSMID 9	9.24e+02	385	5	5.0	259	5	Q23338	2C455.10 PROTEIN.	9.24e+02

386	5	5.0	260	5	015744	PKSB	9.24e+02	459	5	5.0	363	5	023415	SIMILAR TO C. ELEGANS	9.24e+02
387	5	5.0	260	1	026344	SHIKIMATE 5-DEHYDROGEN	9.24e+02	460	5	5.0	364	10	Q04065	CATECHOL O-METHYLTRANS	9.24e+02
388	5	5.0	262	2	Q94DN0	CYSQ PROTEIN (CYSQ).	9.24e+02	461	5	5.0	365	5	Q97366	PRO-PHENOXIDASE ACTI	9.24e+02
389	5	5.0	262	13	Q90713	GALECTIN-3.	9.24e+02	462	5	5.0	366	14	Q90181	VIRAL ENV PROTEIN INTE	9.24e+02
390	5	5.0	263	1	058418	263AA LONG HYPOTHETICA	9.24e+02	463	5	5.0	366	2	Q44163	LIPOPROTEIN PRECURSOR.	9.24e+02
391	5	5.0	265	2	Q92CP3	UBIQUINONE/MENAOINONE	9.24e+02	464	5	5.0	367	2	Q9ZAP9	OUTER MEMBRANE LIPOPRO	9.24e+02
392	5	5.0	265	2	P70831	PERIPLASMIC SUBSTRATE-	9.24e+02	465	5	5.0	367	2	Q44164	LIPOPROTEIN PRECURSOR.	9.24e+02
393	5	5.0	269	5	Q24696	C-TYPE LECTIN-LIKE PRO	9.24e+02	466	5	5.0	369	5	Q19119	F02DB.3 PROTEIN.	9.24e+02
394	5	5.0	270	2	Q34852	PUTATIVE LYSINE-BINDIN	9.24e+02	467	5	5.0	370	14	Q81967	REGULATORY PROTEIN E2.	9.24e+02
395	5	5.0	271	5	Q9XVC6	C27C7.1 PROTEIN.	9.24e+02	468	5	5.0	370	2	Q9X517	NITROUS OXIDE REDUCTAS	9.24e+02
396	5	5.0	272	14	Q9WA93	MATRIX PROTEIN.	9.24e+02	469	5	5.0	371	5	Q9XZV6	G PROTEIN, BETA SUBUNI	9.24e+02
397	5	5.0	273	10	Q65150	OSMOTIC STRESS-INDUCED	9.24e+02	470	5	5.0	371	5	Q18110	T22H2.3 PROTEIN.	9.24e+02
398	5	5.0	273	10	Q82618	T9AA.8 PROTEIN.	9.24e+02	471	5	5.0	371	10	P93142	DIHYDROFLAVONOL REDUCT	9.24e+02
399	5	5.0	276	8	Q9XMU7	RIBOSOMAL PROTEIN S13.	9.24e+02	472	5	5.0	372	5	Q94254	SIMILAR TO TRANSPOSON	9.24e+02
400	5	5.0	277	2	Q927T1	CT504 HYPOTHETICAL PRO	9.24e+02	473	5	5.0	375	2	Q05247	HYPOTHETICAL 42.4 KD P	9.24e+02
401	5	5.0	280	5	Q48843	GENE CLUSTER.	9.24e+02	474	5	5.0	375	10	Q43023	ALCOHOL DEHYDROGENASE	9.24e+02
402	5	5.0	281	5	Q25344	L2759.5 PROTEIN.	9.24e+02	475	5	5.0	375	10	Q43027	ALCOHOL DEHYDROGENASE	9.24e+02
403	5	5.0	283	5	015923	DEOXYRIDINE TRIPOSH	9.24e+02	476	5	5.0	375	2	Q9X514	NITROUS OXIDE REDUCTAS	9.24e+02
404	5	5.0	286	2	P77739	FROM BASES 1798041 TO	9.24e+02	477	5	5.0	375	2	Q9X513	NITROUS OXIDE REDUCTAS	9.24e+02
405	5	5.0	287	2	Q55924	HYPOTHETICAL 31.5 KD P	9.24e+02	478	5	5.0	375	2	Q43022	NITROUS OXIDE REDUCTAS	9.24e+02
406	5	5.0	287	10	Q96307	SIMILAR TO DEHYDROGENA	9.24e+02	479	5	5.0	375	2	Q9X512	NITROUS OXIDE REDUCTAS	9.24e+02
407	5	5.0	288	2	Q07487	HYPOTHETICAL 31.7 KD P	9.24e+02	480	5	5.0	375	10	Q43026	NITROUS OXIDE REDUCTAS	9.24e+02
408	5	5.0	291	10	Q92QT9	WERBP-1 PROTEIN.	9.24e+02	481	5	5.0	375	5	Q45815	ACT-5 PROTEIN.	9.24e+02
409	5	5.0	293	2	Q9X0U0	NADH DEHYDROGENASE, PU	9.24e+02	482	5	5.0	375	2	Q9X429	NITROUS OXIDE REDUCTAS	9.24e+02
410	5	5.0	295	13	Q93528	HOMEOBOX PROTEIN.	9.24e+02	483	5	5.0	375	2	Q9X502	NITROUS OXIDE REDUCTAS	9.24e+02
411	5	5.0	296	14	Q9YLN9	CAPSID PROTEIN VPI (FR	9.24e+02	484	5	5.0	375	10	Q43021	ALCOHOL DEHYDROGENASE	9.24e+02
412	5	5.0	297	10	Q9ZPM4	PEPTIDE TRANSPORTER (F	9.24e+02	485	5	5.0	378	11	Q09010	LUNATIC FRINGE PROTEIN	9.24e+02
413	5	5.0	301	2	Q52907	PHOD PRECURSOR.	9.24e+02	486	5	5.0	379	10	Q65542	HYPOTHETICAL 40.6 KD P	9.24e+02
414	5	5.0	301	6	P79136	F-ACTIN CAPPING PROTEI	9.24e+02	487	5	5.0	379	8	Q63854	CYTCHROME B.	9.24e+02
415	5	5.0	303	14	Q65663	3A PROTEIN.	9.24e+02	488	5	5.0	380	14	Q74432	SURFACE GLYCOPROTEIN (9.24e+02
416	5	5.0	303	10	Q80967	T16B24.22 PROTEIN.	9.24e+02	489	5	5.0	381	3	Q06815	CHROMOSOME XVI COSMID	9.24e+02
417	5	5.0	310	2	Q9ZAI5	HYPOTHETICAL 34.6 KD P	9.24e+02	490	5	5.0	381	5	Q08873	SIMILAR TO GUANINE NUC	9.24e+02
418	5	5.0	313	13	Q9YHF0	AGRIN B19 ISOFORM (FRA	9.24e+02	491	5	5.0	381	2	Q84910	GLYCOSYLTRANSFERASE WB	9.24e+02
419	5	5.0	314	2	Q32102	YUUI PROTEIN.	9.24e+02	492	5	5.0	381	14	Q87392	ENVELOPE GLYCOPROTEIN	9.24e+02
420	5	5.0	315	5	Q26985	D1 PUTATIVE CYSTEINE P	9.24e+02	493	5	5.0	383	14	Q9YP16	ENVELOPE GLYCOPROTEIN	9.24e+02
421	5	5.0	317	5	Q23349	COSMID ZC487.	9.24e+02	494	5	5.0	385	14	Q87296	HYPOTHETICAL 43.8 KD P	9.24e+02
422	5	5.0	318	2	Q95238	CITRATE SYNTHASE (EC 4	9.24e+02	495	5	5.0	385	14	Q87309	ENVELOPE GLYCOPROTEIN	9.24e+02
423	5	5.0	319	4	Q92596	FICOLIN.	9.24e+02	496	5	5.0	386	14	Q87437	ENVELOPE GLYCOPROTEIN	9.24e+02
424	5	5.0	319	5	Q02637	CARBONIC ANHYDRASE (EC	9.24e+02	497	5	5.0	387	2	Q86737	PUTATIVE ADENOSINE DEA	9.24e+02
425	5	5.0	319	2	Q83552	GTP-BINDING PROTEIN (E	9.24e+02	498	5	5.0	388	5	Q01324	F18A11.2 PROTEIN.	9.24e+02
426	5	5.0	319	13	Q93529	FORKEAD-DOMAIN-CONTAI	9.24e+02	499	5	5.0	388	14	Q29592	POLYPROTEIN (FRAGMENT)	9.24e+02
427	5	5.0	319	2	Q34221	PUTATIVE CYCLASE/DEHYD	9.24e+02	500	5	5.0	389	3	Q14001	HYPOTHETICAL 45.1 KD P	9.24e+02
428	5	5.0	319	2	Q9XW16	PUTATIVE PORPHOBILINO	9.24e+02	501	5	5.0	389	10	Q24395	SERINE-THREONINE PROTE	9.24e+02
429	5	5.0	322	2	Q95236	CITRATE SYNTHASE (EC 4	9.24e+02	502	5	5.0	390	14	Q87440	ENVELOPE GLYCOPROTEIN	9.24e+02
430	5	5.0	324	14	Q89914	SC4.	9.24e+02	503	5	5.0	391	14	Q87398	ENVELOPE GLYCOPROTEIN	9.24e+02
431	5	5.0	324	5	Q18412	COSMID C33H5.	9.24e+02	504	5	5.0	392	10	Q96487	ABSCISSION POLYGALACTU	9.24e+02
432	5	5.0	327	5	Q22984	HELIX-FURN-HELIX DNA B	9.24e+02	505	5	5.0	393	14	Q87430	ENVELOPE GLYCOPROTEIN	9.24e+02
433	5	5.0	330	2	Q34308	COMPLEMENT FACTOR H-RE	9.24e+02	506	5	5.0	393	10	Q9ZVX3	ENVELOPE GLYCOPROTEIN	9.24e+02
434	5	5.0	331	4	Q92496	COMPLEMENT FACTOR H-RE	9.24e+02	507	5	5.0	397	10	Q92VX3	F12A24.8 PROTEIN.	9.24e+02
435	5	5.0	333	2	Q9XA89	HYPOTHETICAL 36.1 KD P	9.24e+02	508	5	5.0	397	1	Q93777	397AA LONG HYPOTHETICA	9.24e+02
436	5	5.0	334	5	Q9XVP9	F30A10.5 PROTEIN.	9.24e+02	509	5	5.0	397	4	Q15735	PHOSPHATIDYLINOSITOL (9.24e+02
437	5	5.0	335	11	Q07646	PEGL/MEST PROTEIN.	9.24e+02	510	5	5.0	398	2	Q24939	HYPOTHETICAL 45.3 KD P	9.24e+02
438	5	5.0	336	2	Q25731	GLUCOKINASE (GLK).	9.24e+02	511	5	5.0	399	2	Q9X9W9	PUTATIVE TRANSPORT ASS	9.24e+02
439	5	5.0	336	13	Q98977	COMPLEMENT COMPONENT C	9.24e+02	512	5	5.0	399	5	Q96770	GLUTAMINE SYNTHETASE (9.24e+02
440	5	5.0	337	9	Q38085	HYPOTHETICAL 39.9 KD P	9.24e+02	513	5	5.0	399	11	Q35137	ARISTALESS HOMEOBOX-4	9.24e+02
441	5	5.0	337	2	Q9XDN2	PDUO.	9.24e+02	514	5	5.0	400	14	Q9WJ09	HYPOTHETICAL 44.7 KD P	9.24e+02
442	5	5.0	340	5	P91500	SIMILAR TO MOLYBDENUM	9.24e+02	515	5	5.0	402	4	Q9Y6VA	KIF3 (FRAGMENT)	9.24e+02
443	5	5.0	343	5	Q20245	F40G12.6 PROTEIN.	9.24e+02	516	5	5.0	403	2	Q9WZ11	CREATINASE (EC 3.5.3.3	9.24e+02
444	5	5.0	344	5	P91507	COSMID T28A11.	9.24e+02	517	5	5.0	403	2	Q45380	DNA FOR LIPOPOLYSACCHA	9.24e+02
445	5	5.0	344	2	Q83729	HYPOTHETICAL 37.8 KD P	9.24e+02	518	5	5.0	406	14	Q9WF33	HEMAGGLUTININ (FRAGEN	9.24e+02
446	5	5.0	346	8	Q21215	NADH DEHYDROGENASE SUB	9.24e+02	519	5	5.0	406	14	Q9WF33	HEMAGGLUTININ (FRAGEN	9.24e+02
447	5	5.0	346	8	Q21124	NADH DEHYDROGENASE SUB	9.24e+02	520	5	5.0	408	2	Q83830	HYPOHETICAL 43.4 KD P	9.24e+02
448	5	5.0	346	8	Q21144	NADH DEHYDROGENASE SUB	9.24e+02	521	5	5.0	409	5	Q24080	DSHC.	9.24e+02
449	5	5.0	347	8	Q21195	NADH DEHYDROGENASE SUB	9.24e+02	522	5	5.0	409	5	Q19414	F13E9.4 PROTEIN.	9.24e+02
450	5	5.0	347	8	Q21211	NADH DEHYDROGENASE SUB	9.24e+02	523	5	5.0	412	14	Q65354	ORF C (FRAGMENT).	9.24e+02
451	5	5.0	347	8	Q21675	NADH DEHYDROGENASE SUB	9.24e+02	524	5	5.0	412	14	P74200	PENICILLIN-BINDING PRO	9.24e+02
452	5	5.0	348	8	Q21305	NADH DEHYDROGENASE SUB	9.24e+02	525	5	5.0	415	6	Q28177	PHAKIN.	9.24e+02
453	5	5.0	349	2	Q92Z53	NADH DEHYDROGENASE SUB	9.24e+02	526	5	5.0	415	11	Q9Z0K4	INTERLEUKIN-5 RECEPT	9.24e+02
454	5	5.0	351	5	Q45372	NADP-DEPENDENT ALCOHOL	9.24e+02	527	5	5.0	416	14	Q9Y986	VIRAL RNA-DEPENDENT RN	9.24e+02
455	5	5.0	355	4	Q9Y5W3	F15H9.2 PROTEIN.	9.24e+02	528	5	5.0	416	5	Q16353	F13H6.5 PROTEIN.	9.24e+02
456	5	5.0	355	4	P87046	KRUPPEL-LIKE ZINC FING	9.24e+02	529	5	5.0	417	4	Q43820	SIMILAR TO HYALURONOGL	9.24e+02
457	5	5.0	360	10	Q82391	OXYSTEROL-BINDING PROT	9.24e+02	530	5	5.0	418	5	Q17239	K10B4.4 PROTEIN.	9.24e+02
458	5	5.0	361	1	Q59364	T27A16.26 PROTEIN.	9.24e+02	531	5	5.0	418	2	Q9X2H0	SUGAR ABC TRANSPORTER,	9.24e+02
						361AA LONG HYPOTHETICA	9.24e+02								

532	5	5.0	419 14	P87662	TRANSCRIPTIONAL PROTEI	9.24e+02	605	5	5.0	505 5	001328	F4GAB.2 PROTEIN.	9.24e+02
533	5	5.0	420 2	O68526	SYMBIOSIS ISLAND INTEG	9.24e+02	606	5	5.0	506 5	Q23576	SIMILAR TO SODIUM/PHOP	9.24e+02
534	5	5.0	420 14	O9YPP5	MBV AUSTRALIAN ISOLATE	9.24e+02	607	5	5.0	507 11	O62720	ZNT-1.	9.24e+02
535	5	5.0	420 11	O9WV60	GLYCOCEN SYNTHASE KINA	9.24e+02	608	5	5.0	510 5	O44382	SLMB.	9.24e+02
536	5	5.0	420 15	O19624	COSMID F20B4.	9.24e+02	609	5	5.0	510 3	O93992	HYPOTHETICAL MEMBRANE	9.24e+02
537	5	5.0	421 13	O19H60	GLYCOCEN SYNTHASE KINA	9.24e+02	610	5	5.0	511 14	O89664	(STRAIN 87-VC-B).	9.24e+02
538	5	5.0	421 10	O39048	CER2 GENE.	9.24e+02	611	5	5.0	511 14	O89000	(STRAIN 86-DF-P) GLYCO	9.24e+02
539	5	5.0	422 4	O9Y353	SOLUBLE LIVER ANTIGEN/	9.24e+02	612	5	5.0	511 14	O89625	(STRAIN 83-HD-B1).	9.24e+02
540	5	5.0	424 10	O41109	REGULATOR OF MAT2.	9.24e+02	613	5	5.0	511 14	O88996	(STRAIN 84-PN-H) GLYCO	9.24e+02
541	5	5.0	426 2	O67578	FLAGELLAR HOOK ASSOCIA	9.24e+02	614	5	5.0	511 14	O89007	(STRAIN 84-PN-B2) GLYC	9.24e+02
542	5	5.0	428 2	O92975	ATPASE.	9.24e+02	615	5	5.0	511 14	O89008	(STRAIN 85-ES-B2) GLYC	9.24e+02
543	5	5.0	431 2	O45081	MOPA.	9.24e+02	616	5	5.0	513 2	O48246	VACUOLATING CITOTOXIN	9.24e+02
544	5	5.0	435 4	O13309	CYCLIN A/CDK2-ASSOCIAT	9.24e+02	617	5	5.0	513 2	O9WZ23	2-ISOPROPYLMALATE SYNT	9.24e+02
545	5	5.0	437 5	O18379	DOPA DECARBOXYLASE (DD	9.24e+02	618	5	5.0	513 14	O88094	GLYCOPROTEIN 120.	9.24e+02
546	5	5.0	437 2	O57387	HASA, HASD AND HASE GE	9.24e+02	619	5	5.0	516 14	O87970	GLYCOPROTEIN 120.	9.24e+02
547	5	5.0	439 1	O9Y689	HYPOTHETICAL 50.9 KD P	9.24e+02	620	5	5.0	516 10	O65313	HYPOTHETICAL 56.3 KD P	9.24e+02
548	5	5.0	441 2	O07386	HISTIDINE KINASE.	9.24e+02	621	5	5.0	517 5	O96509	AXONEMAL DYNEIN INTERM	9.24e+02
549	5	5.0	443 2	O34417	METALLOPROTEASE TRANSP	9.24e+02	622	5	5.0	518 2	O34512	YFMM PROTEIN.	9.24e+02
550	5	5.0	445 10	O41337	FEEBLY.	9.24e+02	623	5	5.0	518 3	O59896	LACCASE PRECURSOR (EC	9.24e+02
551	5	5.0	446 6	O19071	ALPHA-1,6-MANNOSYL-GLY	9.24e+02	624	5	5.0	519 2	O9X991	FRUB.	9.24e+02
552	5	5.0	448 11	O9WVH8	DEVELOPMENTAL ARTERIES	9.24e+02	625	5	5.0	520 5	O45317	Y17D7A.4 PROTEIN.	9.24e+02
553	5	5.0	448 14	O83457	FIBRE.	9.24e+02	626	5	5.0	521 14	O87462	ENVELOPE GLYCOPROTEIN	9.24e+02
554	5	5.0	448 2	O92N97	BETA-GLUCOSIDASE.	9.24e+02	627	5	5.0	521 14	O87463	ENVELOPE GLYCOPROTEIN	9.24e+02
555	5	5.0	450 13	O90809	INTERMEDIATE FILAMENT	9.24e+02	628	5	5.0	522 2	O55984	HYPOTHETICAL 58.4 KD P	9.24e+02
556	5	5.0	452 1	O29870	ACETYL-COA DECARBONYLA	9.24e+02	629	5	5.0	522 14	O87465	ENVELOPE GLYCOPROTEIN	9.24e+02
557	5	5.0	452 14	O07045	D6L PROTEIN.	9.24e+02	630	5	5.0	522 14	O87466	ENVELOPE GLYCOPROTEIN	9.24e+02
558	5	5.0	454 4	O9Y2T3	GUANINE DEAMINASE GDA.	9.24e+02	631	5	5.0	523 10	O92V69	PUTATIVE UBIQUITIN ACT	9.24e+02
559	5	5.0	455 8	O47056	RIBULOSE BISPHOSPHATE	9.24e+02	632	5	5.0	524 14	O87454	ENVELOPE GLYCOPROTEIN	9.24e+02
560	5	5.0	455 10	O92V41	F9K20.13 PROTEIN.	9.24e+02	633	5	5.0	525 14	O87460	ENVELOPE GLYCOPROTEIN	9.24e+02
561	5	5.0	455 2	O9X479	ENTD.	9.24e+02	634	5	5.0	525 14	O87466	ENVELOPE GLYCOPROTEIN	9.24e+02
562	5	5.0	460 5	O22106	SIMILAR TO ACETLY-COA	9.24e+02	635	5	5.0	525 14	O87455	ENVELOPE GLYCOPROTEIN	9.24e+02
563	5	5.0	462 2	O52801	PCZA361.14.	9.24e+02	636	5	5.0	526 4	O75567	RAF RESPONSIVE ZINC FI	9.24e+02
564	5	5.0	463 4	O60540	HYALURONIDASE.	9.24e+02	637	5	5.0	527 14	O87458	ENVELOPE GLYCOPROTEIN	9.24e+02
565	5	5.0	465 2	O51601	2-HALOENZOATE 1,2-DIO	9.24e+02	638	5	5.0	527 14	O87468	ENVELOPE GLYCOPROTEIN	9.24e+02
566	5	5.0	467 5	O16315	C05C8.7 PROTEIN.	9.24e+02	639	5	5.0	530 10	O04892	CYTOCHROME P450 LIKE.T	9.24e+02
567	5	5.0	467 8	O33404	RIBULOSE BISPHOSPHATE	9.24e+02	640	5	5.0	531 4	Q15043	KIAA0062 PROTEIN (FRAG	9.24e+02
568	5	5.0	469 5	O20752	F54C9.2 PROTEIN.	9.24e+02	641	5	5.0	531 3	O74858	LYSLY-TRNA SYNTHETASE.	9.24e+02
569	5	5.0	469 8	P94057	RIBULOSE BISPHOSPHATE	9.24e+02	642	5	5.0	531 10	O82416	TYROSINE/DOPA DECARBOX	9.24e+02
570	5	5.0	470 14	O9WSX5	UL38 PROTEIN.	9.24e+02	643	5	5.0	531 10	O43014	BETA-GLUCOSIDASE (EC 3	9.24e+02
571	5	5.0	471 2	O83871	CONSERVED HYPOTHETICAL	9.24e+02	644	5	5.0	532 10	O81849	HYPOTHETICAL 60.3 KD P	9.24e+02
572	5	5.0	471 10	O9XIB2	F13P21.11 PROTEIN.	9.24e+02	645	5	5.0	535 2	O56676	MANNOSE-SENSITIVE HEMA	9.24e+02
573	5	5.0	472 5	O95656	HYPOTHETICAL 52.6 KD P	9.24e+02	646	5	5.0	535 2	O59141	CHITINASE PRECURSOR (E	9.24e+02
574	5	5.0	473 5	O20924	F57B1.2 PROTEIN.	9.24e+02	647	5	5.0	542 2	O86368	FADE8.	9.24e+02
575	5	5.0	474 11	O9WUM4	CORONIN-3.	9.24e+02	648	5	5.0	543 5	O20720	F53F4.11 PROTEIN.	9.24e+02
576	5	5.0	475 8	O32088	RIBULOSE BISPHOSPHATE	9.24e+02	649	5	5.0	543 5	O14879	MUCIN (FRAGMENT).	9.24e+02
577	5	5.0	476 8	O37734	RIBULOSE BISPHOSPHATE	9.24e+02	650	5	5.0	543 5	O45069	C11D2.4 PROTEIN.	9.24e+02
578	5	5.0	478 2	O86666	PUTATIVE SUGAR TRANSFE	9.24e+02	651	5	5.0	544 10	O22915	G-BETA-REPEAT CONTAINI	9.24e+02
579	5	5.0	481 14	O9WRJ0	ENVELOPE GLYCOPROTEIN	9.24e+02	652	5	5.0	545 5	O27621	CARBOXYLESTERASE (EC 3	9.24e+02
580	5	5.0	483 1	O58952	483AA LONG HYPOTHETICA	9.24e+02	653	5	5.0	548 5	O16177	ESTERASE 5A PRECURSOR	9.24e+02
581	5	5.0	483 10	O40490	CYCLIN A-LIKE PROTEIN.	9.24e+02	654	5	5.0	550 4	O43405	COCH-5B2.	9.24e+02
582	5	5.0	483 5	O22698	SIMILAR TO GLYCOSYLTRA	9.24e+02	655	5	5.0	553 14	O9WF46	FUSION GLYCOPROTEIN PR	9.24e+02
583	5	5.0	485 11	O35667	MAX DIMERIZATION PROTE	9.24e+02	656	5	5.0	553 14	O9WI28	F PROTEIN.	9.24e+02
584	5	5.0	485 2	O9X390	PX01-133.	9.24e+02	657	5	5.0	553 2	O9ZJ35	PUTATIVE.	9.24e+02
585	5	5.0	486 2	O84116	HYPOTHETICAL 55.2 KD P	9.24e+02	658	5	5.0	553 14	O83847	FUSION GLYCOPROTEIN PR	9.24e+02
586	5	5.0	486 10	O04591	SEQUENCE OF BAC F19K23	9.24e+02	659	5	5.0	554 5	O44089	ZK994.1 PROTEIN.	9.24e+02
587	5	5.0	486 10	O22909	HYPOTHETICAL PROTEIN.	9.24e+02	660	5	5.0	559 2	O83432	APOLIPOPROTEIN N-ACYLT	9.24e+02
588	5	5.0	487 2	P94412	HOMOLOGUE OF HYPOTHEI	9.24e+02	661	5	5.0	560 14	O9WQW9	HEMAGGLUTININ (FRAGMEN	9.24e+02
589	5	5.0	487 2	P72269	ORF8.	9.24e+02	662	5	5.0	560 11	O62634	BRAIN SPECIFIC NA+-DEP	9.24e+02
590	5	5.0	489 14	O9WBL2	NUCLEOCAPSID PROTEIN.	9.24e+02	663	5	5.0	561 5	O76134	NRK-RELATED KINASE.	9.24e+02
591	5	5.0	489 14	O9WJ25	ORF OP-1.	9.24e+02	664	5	5.0	562 14	O67140	HEMAGGLUTININ.	9.24e+02
592	5	5.0	489 14	O9WMM9	NUCLEOCAPSID PROTEIN.	9.24e+02	665	5	5.0	562 14	O67143	HEMAGGLUTININ.	9.24e+02
593	5	5.0	489 2	O54980	PROLINE PERMEASE (FRAG	9.24e+02	666	5	5.0	562 14	O67144	HEMAGGLUTININ.	9.24e+02
594	5	5.0	489 14	O88107	SURFACE ENVELOPE GLYCO	9.24e+02	667	5	5.0	562 14	O67016	HEMAGGLUTININ.	9.24e+02
595	5	5.0	489 2	O47553	PROLINE PERMEASE (FRAG	9.24e+02	668	5	5.0	562 14	O67011	HEMAGGLUTININ.	9.24e+02
596	5	5.0	490 2	O9W779	UDP-N-ACETYLMURAMOYLAL	9.24e+02	669	5	5.0	562 14	O67326	HEMAGGLUTININ.	9.24e+02
597	5	5.0	490 5	O45920	Y37A1A.3 PROTEIN.	9.24e+02	670	5	5.0	562 14	O67327	HEMAGGLUTININ.	9.24e+02
598	5	5.0	490 14	O88120	SURFACE ENVELOPE GLYCO	9.24e+02	671	5	5.0	562 14	O67120	HEMAGGLUTININ.	9.24e+02
599	5	5.0	491 2	O51279	HEAT SHOCK PROTEIN 70	9.24e+02	672	5	5.0	562 14	O67123	HEMAGGLUTININ.	9.24e+02
600	5	5.0	494 13	O73621	UTROPHIN (DYSTROPHIN-R	9.24e+02	673	5	5.0	564 14	O72736	A54R PROTEIN.	9.24e+02
601	5	5.0	495 10	O92UX1	PUTATIVE CYTOCHROME P4	9.24e+02	674	5	5.0	565 14	O88254	F PROTEIN.	9.24e+02
602	5	5.0	495 10	O22217	T32G6.7 PROTEIN.	9.24e+02	675	5	5.0	565 14	O88259	F PROTEIN.	9.24e+02
603	5	5.0	497 2	O51503	HYPOTHETICAL 59.3 KD P	9.24e+02	676	5	5.0	566 14	O9WCE6	HEMAGGLUTININ PRECURSO	9.24e+02
604	5	5.0	503 14	O9W754	U10 PROTEIN.	9.24e+02	677	5	5.0	566 14	O9WCE4	HEMAGGLUTININ PRECURSO	9.24e+02

678	5	5.0	566 14	Q9WCE8	HEMAGGLUTININ PRECURSO	9.24e+02	751	5	5.0	642 3	Q9Y7T0	HYPOHETICAL DNAJ DOMA	9.24e+02
679	5	5.0	566 14	Q9WCE3	HEMAGGLUTININ PRECURSO	9.24e+02	752	5	5.0	642 2	P76016	DHAR PROTEIN.	9.24e+02
680	5	5.0	566 14	Q9WCE2	HEMAGGLUTININ PRECURSO	9.24e+02	753	5	5.0	645 5	Q09478	PUTATIVE 70.0 KD ZINC	9.24e+02
681	5	5.0	566 14	Q9WCE5	HEMAGGLUTININ PRECURSO	9.24e+02	754	5	5.0	650 5	Q02306	T09E11.4 PROTEIN.	9.24e+02
682	5	5.0	566 14	Q9WCD9	HEMAGGLUTININ PRECURSO	9.24e+02	755	5	5.0	655 5	Q04832	HYDROGENOSOMAL CHAPERO	9.24e+02
683	5	5.0	566 14	Q9WCD8	HEMAGGLUTININ PRECURSO	9.24e+02	756	5	5.0	660 2	O25815	CONSERVED HYPOHETICAL	9.24e+02
684	5	5.0	566 14	Q9WCE1	HEMAGGLUTININ PRECURSO	9.24e+02	757	5	5.0	660 14	O41172	ENV.	9.24e+02
685	5	5.0	566 14	Q9WCE0	HEMAGGLUTININ PRECURSO	9.24e+02	758	5	5.0	661 10	O22577	ARM REPEAT CONTAINING	9.24e+02
686	5	5.0	566 14	Q9WCE7	HEMAGGLUTININ PRECURSO	9.24e+02	759	5	5.0	662 5	P91331	COSMID F54H5.	9.24e+02
687	5	5.0	566 14	Q9WCF2	HEMAGGLUTININ.	9.24e+02	760	5	5.0	662 5	Q09512	HYPOHETICAL 76.7 KD P	9.24e+02
688	5	5.0	566 11	Q62977	MITOGEN-ACTIVATED ZINC	9.24e+02	761	5	5.0	664 10	O49319	PUTATIVE POLYGALACTURO	9.24e+02
689	5	5.0	566 2	O32309	NEUTRAL PROTEASE A.	9.24e+02	762	5	5.0	669 2	Q56151	P-AMINOBENZOIC ACID SY	9.24e+02
690	5	5.0	566 14	O89459	HEMAGGLUTININ.	9.24e+02	763	5	5.0	673 4	O49859	KIAA0759 PROTEIN (FRAG	9.24e+02
691	5	5.0	566 14	O84114	HEMAGGLUTININ.	9.24e+02	764	5	5.0	675 2	O87906	INSECTICIDAL PROTEIN J	9.24e+02
692	5	5.0	566 14	O82770	HEMAGGLUTININ.	9.24e+02	765	5	5.0	683 14	O11780	TRANSFORMING GROWTH FA	9.24e+02
693	5	5.0	566 14	O98095	HEMAGGLUTININ.	9.24e+02	766	5	5.0	683 10	Q9Z046	PUTATIVE COPIA-LIKE RE	9.24e+02
694	5	5.0	566 14	O98094	HEMAGGLUTININ.	9.24e+02	767	5	5.0	690 5	Q9XUC6	M162.7 PROTEIN.	9.24e+02
695	5	5.0	566 14	O98092	HEMAGGLUTININ.	9.24e+02	768	5	5.0	690 3	Q74874	PUTATIVE TRANSCRIPTION	9.24e+02
696	5	5.0	566 4	O60273	KIAA0520 PROTEIN (FRAG	9.24e+02	769	5	5.0	693 5	O61920	C18G1.4 PROTEIN.	9.24e+02
697	5	5.0	569 4	Q9Y213	BETA-TRANSDUCIN REPEAT	9.24e+02	770	5	5.0	694 14	Q9YNA9	ENV PROTEIN.	9.24e+02
698	5	5.0	570 3	Q06150	CHROMOSOME XII COSMID	9.24e+02	771	5	5.0	696 5	O17034	ENV PROTEIN.	9.24e+02
699	5	5.0	571 14	Q9YX78	HN HEMAGGLUTININ-NURAM	9.24e+02	772	5	5.0	697 3	O74504	IMMUNE FACTOR.	9.24e+02
700	5	5.0	571 14	Q9YX79	HN HEMAGGLUTININ-NURAM	9.24e+02	773	5	5.0	698 8	O98651	HYPOHETICAL 77.8 KD P	9.24e+02
701	5	5.0	571 14	Q9W919	HEMAGGLUTININ-NEURAMIN	9.24e+02	774	5	5.0	698 8	O98642	NADH DEHYDROGENASE SUB	9.24e+02
702	5	5.0	571 14	Q9W9B1	HEMAGGLUTININ-NEURAMIN	9.24e+02	775	5	5.0	699 14	Q69384	ENV MRNA.	9.24e+02
703	5	5.0	571 14	Q9W9C3	HEMAGGLUTININ-NEURAMIN	9.24e+02	776	5	5.0	701 2	O87792	POLYRIBONUCLEOTIDE NUC	9.24e+02
704	5	5.0	571 14	Q9W9C2	HEMAGGLUTININ-NEURAMIN	9.24e+02	777	5	5.0	701 2	O86073	POLYPHOSPHATE KINASE.	9.24e+02
705	5	5.0	571 14	Q9W129	HN PROTEIN.	9.24e+02	778	5	5.0	702 2	O86988	POLYRIBONUCLEOTIDE NUC	9.24e+02
706	5	5.0	571 14	Q9Y851	HEMAGGLUTININ-NEURAMIN	9.24e+02	779	5	5.0	702 2	O86988	POLYPHOSPHATE KINASE.	9.24e+02
707	5	5.0	574 14	Q9Y824	FUSION GLYCOPROTEIN PR	9.24e+02	780	5	5.0	710 5	Q96694	KINESIN FAMILY MEMBER	9.24e+02
708	5	5.0	574 10	O89535	FUSION GLYCOPROTEIN PR	9.24e+02	781	5	5.0	710 5	Q96694	UMOB.	9.24e+02
709	5	5.0	574 10	O80459	PUTATIVE NICOTINATE PH	9.24e+02	782	5	5.0	711 2	Q9WYS9	1-DEOXY-D-XYLULOSE 5-P	9.24e+02
710	5	5.0	576 14	O41623	ENVELOPE GLYCOPROTEIN	9.24e+02	783	5	5.0	711 11	O88679	HYPOHETICAL 80.9 KD P	9.24e+02
711	5	5.0	576 14	Q86677	HEMAGGLUTININ (FRAGMEN	9.24e+02	784	5	5.0	712 5	O87469	TRIP PROTEIN (FRAGMENT	9.24e+02
712	5	5.0	577 14	Q9W9C3	HEMAGGLUTININ-NEURAMIN	9.24e+02	785	5	5.0	712 5	O87469	FIBULIN-1 ISOFORM C PR	9.24e+02
713	5	5.0	577 14	Q9W9H0	HEMAGGLUTININ-NEURAMIN	9.24e+02	786	5	5.0	714 3	Q08119	CHROMOSOME XV READING	9.24e+02
714	5	5.0	577 14	Q9W9B1	HEMAGGLUTININ-NEURAMIN	9.24e+02	787	5	5.0	720 2	Q92876	GLUCAN BRANCHING ENZYM	9.24e+02
715	5	5.0	577 14	Q9W9B2	HEMAGGLUTININ-NEURAMIN	9.24e+02	788	5	5.0	725 10	Q96659	TETRAFUNCTIONAL PROTEIN	9.24e+02
716	5	5.0	577 14	Q9W9B3	HEMAGGLUTININ-NEURAMIN	9.24e+02	789	5	5.0	735 1	O26457	CONSERVED PROTEIN.	9.24e+02
717	5	5.0	581 14	Q93850	HAEMAGGLUTININ-NEURAMI	9.24e+02	790	5	5.0	745 1	Q9Y9L3	745AA LONG HYPOHETICA	9.24e+02
718	5	5.0	583 3	Q12372	CHROMOSOME XII READING	9.24e+02	791	5	5.0	748 14	Q9YR01	COS54.1 PRECURSOR (FRA	9.24e+02
719	5	5.0	586 2	Q9WX29	PUTATIVE ARGINYL-TRNA	9.24e+02	792	5	5.0	748 2	O35260	CAG PATHOGENICITY ISLA	9.24e+02
720	5	5.0	587 3	O25510	OUTER MEMBRANE PROTEIN	9.24e+02	793	5	5.0	749 5	Q02602	ENVELOPE GLYCOPROTEIN	9.24e+02
721	5	5.0	589 3	Q08295	CHROMOSOME XV READING	9.24e+02	794	5	5.0	758 4	Q16891	HYPOHETICAL PROTEIN I	9.24e+02
722	5	5.0	589 2	P96439	EXPDL.	9.24e+02	795	5	5.0	758 4	Q16891	MOTOR PROTEIN.	9.24e+02
723	5	5.0	590 2	Q9ZMY8	PUTATIVE.	9.24e+02	796	5	5.0	759 3	O14267	HYPOHETICAL 83.4 KD P	9.24e+02
724	5	5.0	592 11	Q9WY88	SODIUM-COUPLED ASCORBI	9.24e+02	797	5	5.0	762 5	O27701	SIALIDASE L PRECURSOR	9.24e+02
725	5	5.0	593 13	Q9W677	LIM DOMAIN INTERACTING	9.24e+02	798	5	5.0	771 11	P97691	INS-1 WINGED HELIX.	9.24e+02
726	5	5.0	594 11	O88402	SYNAPTOJANIN 2 ISOFORM	9.24e+02	799	5	5.0	774 2	O23880	HYPOHETICAL 83.8 KD P	9.24e+02
727	5	5.0	595 2	O57525	2-SUCCINYL-6-HYDROXY-2	9.24e+02	800	5	5.0	774 5	Q23424	CODED FOR BY C. ELEGAN	9.24e+02
728	5	5.0	599 3	Q10988	UV-ENDORNUCLASE.	9.24e+02	801	5	5.0	780 10	O04346	REGULATORY PROTEIN VIV	9.24e+02
729	5	5.0	601 5	O77459	KEN PROTEIN.	9.24e+02	802	5	5.0	784 4	O60402	SP4 TRANSCRIPTION FACT	9.24e+02
730	5	5.0	606 2	O66380	SPAA.	9.24e+02	803	5	5.0	802 8	O35062	COXI INTRON2 ORF.	9.24e+02
731	5	5.0	609 4	Q12886	CALCIUM-ACTIVATED POTA	9.24e+02	804	5	5.0	803 3	O74964	BROMODOMAIN PROTEIN.	9.24e+02
732	5	5.0	610 2	O51577	EXODEOXYRIBONUCLEASE V	9.24e+02	805	5	5.0	807 4	O94886	KIAA0792 PROTEIN.	9.24e+02
733	5	5.0	614 5	O46149	WEEL-LIKE KINASE.	9.24e+02	806	5	5.0	808 5	Q18098	COSMID C18F10.	9.24e+02
734	5	5.0	615 14	Q93758	HEMAGGLUTININ-NEURAMIN	9.24e+02	807	5	5.0	821 11	Q61161	RAB8 INTERACTING PROTE	9.24e+02
735	5	5.0	616 14	Q93852	HEMAGGLUTININ-NEURAMIN	9.24e+02	808	5	5.0	822 2	Q9ZHG7	HYPOHETICAL 92.4 KD P	9.24e+02
736	5	5.0	616 14	Q84837	ORE 3 (FRAGMENT).	9.24e+02	809	5	5.0	828 3	O74240	CELLOBIOSE DEHYDROGENA	9.24e+02
737	5	5.0	617 5	Q9XWZ2	Y45F3A.3 PROTEIN.	9.24e+02	810	5	5.0	828 2	O68107	HYPOHETICAL 86.4 KD P	9.24e+02
738	5	5.0	618 5	Q18693	F28F8-2 PROTEIN.	9.24e+02	811	5	5.0	830 4	Q14162	HYPOHETICAL 86.4 KD P	9.24e+02
739	5	5.0	619 4	O75358	NEUROAN1.	9.24e+02	812	5	5.0	832 4	Q9YPU5	KIAA0149 PROTEIN.	9.24e+02
740	5	5.0	620 5	O16519	T05H4.14 PROTEIN.	9.24e+02	813	5	5.0	834 11	O88941	DNA POLYMERASE.	9.24e+02
741	5	5.0	620 10	O81008	PUTATIVE AMINO-ACID AC	9.24e+02	814	5	5.0	835 2	O25908	GLYCOPROTEIN PROCESSIN	9.24e+02
742	5	5.0	623 5	Q27560	SERINE/THREONINE PROTE	9.24e+02	815	5	5.0	837 4	O3Y488	PUTATIVE ADENINE SPECI	9.24e+02
743	5	5.0	624 5	O61393	GLY5C (EC 2.4.1.41) (P	9.24e+02	816	5	5.0	838 9	O64330	HYPOHETICAL 91.8 KD P	9.24e+02
744	5	5.0	626 5	O61392	GLY5B (EC 2.4.1.41) (P	9.24e+02	817	5	5.0	842 10	O49527	GP16.	9.24e+02
745	5	5.0	629 10	Q39174	PUTATIVE ALCOHOL DEHYD	9.24e+02	818	5	5.0	843 14	Q03766	POLLEN-SPECIFIC PROTEI	9.24e+02
746	5	5.0	633 11	P70419	UDP-GALNAC:POLYPEPTIDE	9.24e+02	819	5	5.0	845 10	O49289	DNA POLYMERASE (EC 2.7	9.24e+02
747	5	5.0	633 14	Q65863	FUSION PROTEIN (FRAGME	9.24e+02	820	5	5.0	845 3	O94719	SIMILAR ATP-DEPENDENT	9.24e+02
748	5	5.0	634 5	Q17474	B0334.3A PROTEIN.	9.24e+02	821	5	5.0	853 1	O30772	HYPOHETICAL 94.5 KD P	9.24e+02
749	5	5.0	639 13	Q01707	CONVERTASE PC2.	9.24e+02	822	5	5.0	858 14	O74114	AMYLOPULLULANASE.	9.24e+02
750	5	5.0	640 14	Q9WAT4	MINOR CORE PROTEIN VP4	9.24e+02	823	5	5.0	862 14	Q9WQ12	GP160.	9.24e+02
			641 5	Q9Y026	BCDNA.LD22679.	9.24e+02				862 14	Q9WLD7	ENV POLYPROTEIN.	9.24e+02
												ENVELOPE GLYCOPROTEIN.	9.24e+02

824	5	5.0	865	14	Q9WIU7	ENVELOPE GLYCOPROTEIN	9.24e+02	897	5	5.0	1102	2	P95684	SUBTILISIN-LIKE PROTEA	9.24e+02
825	5	5.0	865	14	Q9WIU3	ENVELOPE GLYCOPROTEIN	9.24e+02	898	5	5.0	1110	13	Q91255	NF-180.	9.24e+02
826	5	5.0	865	14	Q9WIU5	ENVELOPE GLYCOPROTEIN	9.24e+02	899	5	5.0	1115	14	Q83484	130 KD PROTEIN.	9.24e+02
827	5	5.0	865	14	Q9WIU4	ENVELOPE GLYCOPROTEIN	9.24e+02	900	5	5.0	1119	5	Q77374	PFC0810C PROTEIN.	9.24e+02
828	5	5.0	865	14	Q9WIU8	ENVELOPE GLYCOPROTEIN	9.24e+02	901	5	5.0	1123	14	Q66933	POLYMERASE (FRAGMENT).	9.24e+02
829	5	5.0	867	2	Q9XBS2	MEMBRANE ALANYL AMINOP	9.24e+02	902	5	5.0	1128	11	Q88442	AORTIC CARBOXYPEPTIDAS	9.24e+02
830	5	5.0	871	5	Q76976	SUDF98 PROTEIN.	9.24e+02	903	5	5.0	1132	14	Q07022	M POLYPROTEIN PRECURSO	9.24e+02
831	5	5.0	873	4	Q9V652	VITAMIN D RECEPTOR-INT	9.24e+02	904	5	5.0	1137	13	Q9W6F6	M POLYPROTEIN TYROSINE KINA	9.24e+02
832	5	5.0	877	14	Q55596	PUTATIVE DNA-DIRECTED	9.24e+02	905	5	5.0	1138	2	Q84133	(POSSIBLE TRANSMEMBRAN	9.24e+02
833	5	5.0	878	10	Q42704	LIPOKYGENASE 1 (EC 1.1	9.24e+02	906	5	5.0	1140	5	Q10028	PUTATIVE GUANYLATE CYC	9.24e+02
834	5	5.0	879	3	Q07807	CHROMOSOME XII READING	9.24e+02	907	5	5.0	1140	11	Q9WV39	DAMAGE-SPECIFIC DNA BI	9.24e+02
835	5	5.0	880	14	Q03820	ENVELOPE POLYPROTEIN G	9.24e+02	908	5	5.0	1142	14	Q9WVG2	M POLYPROTEIN.	9.24e+02
836	5	5.0	884	2	Q9XBA6	SENSOR PROTEIN KOPD (F	9.24e+02	909	5	5.0	1144	14	Q9WVK6	M POLYPROTEIN.	9.24e+02
837	5	5.0	885	2	Q9X2W8	PPH.	9.24e+02	910	5	5.0	1191	11	Q97690	BASMENT MEMBRANE-ASSO	9.24e+02
838	5	5.0	885	3	Q07533	CHROMOSOME IV READING	9.24e+02	911	5	5.0	1194	4	Q94965	KIAA0890 PROTEIN.	9.24e+02
839	5	5.0	888	5	Q04135	PUTATIVE RNA-DIRECTED	9.24e+02	912	5	5.0	1203	14	Q98815	POL POLYPROTEIN (FRAGM	9.24e+02
840	5	5.0	891	1	Q93635	STETTERLYSIN (FRAGMENT	9.24e+02	913	5	5.0	1206	11	Q9WTK6	ENDOTHELIAL NITRIC OXI	9.24e+02
841	5	5.0	893	13	Q9W6J4	TRANSCRIPTION FACTOR C	9.24e+02	914	5	5.0	1215	4	Q75161	KIAA0673 PROTEIN (FRAG	9.24e+02
842	5	5.0	902	8	Q35063	COXI INTRON1 ORF.	9.24e+02	915	5	5.0	1216	11	Q88404	SYNAPTOJANIN 2 ISOFORM	9.24e+02
843	5	5.0	903	5	Q17917	E02H4.3 PROTEIN.	9.24e+02	916	5	5.0	1219	4	Q15242	NRD2 CONVERTASE (EC 3.	9.24e+02
844	5	5.0	905	14	P87562	HEXON PROTEIN.	9.24e+02	917	5	5.0	1222	2	Q9X349	PX01-79.	9.24e+02
845	5	5.0	914	9	Q9XJB1	PUTATIVE TAIL-HOST SPE	9.24e+02	918	5	5.0	1224	5	Q96209	HYPOTHETICAL 144.0 KD	9.24e+02
846	5	5.0	917	14	Q9WS58	REVERSE TRANSCRIPTASE.	9.24e+02	919	5	5.0	1229	11	Q35836	NRD2 CONVERTASE (EC 3.	9.24e+02
847	5	5.0	917	14	Q9WI15	POL.	9.24e+02	920	5	5.0	1243	11	Q55180	RAT-SLOWPOKE-ALPHA.	9.24e+02
848	5	5.0	917	4	Q43444	HEXOKINASE I (EC 2.7.7	9.24e+02	921	5	5.0	1261	5	Q45380	T23F1.5 PROTEIN.	9.24e+02
849	5	5.0	919	14	Q9WPP0	ENVELOPE GLYCOPROTEIN.	9.24e+02	922	5	5.0	1262	5	Q18117	PUTATIVE G-BETA-REPEAT	9.24e+02
850	5	5.0	928	2	Q9SG10	PUTATIVE TRANSCRIPTION	9.24e+02	923	5	5.0	1269	10	Q02269	GAM1 GENE.	9.24e+02
851	5	5.0	931	10	Q04026	HYPOTHETICAL 104.6 KD	9.24e+02	924	5	5.0	1287	5	Q26178	MULTIDRUG RESISTANCE P	9.24e+02
852	5	5.0	934	1	Q73954	DNA TOPOISOMERASE I (F	9.24e+02	925	5	5.0	1287	13	Q91586	VACUOLATING CYTOTOXIN	9.24e+02
853	5	5.0	940	14	Q69518	SIMILAR TO MCWV IE2.	9.24e+02	926	5	5.0	1291	2	Q92HU7	MAJOR CAPSID PROTEIN.	9.24e+02
854	5	5.0	940	14	Q56303	HYPOTHETICAL 107.6 KD	9.24e+02	927	5	5.0	1291	9	Q64295	HYPOTHETICAL 144.3 KD	9.24e+02
855	5	5.0	941	2	Q92485	110 KDA XYLANASE PRECU	9.24e+02	928	5	5.0	1302	4	Q43305	KIAA0421 (FRAGMENT).	9.24e+02
856	5	5.0	948	5	Q22155	T04C10.1 PROTEIN.	9.24e+02	929	5	5.0	1308	11	Q922N7	RECEPTOR TYROSINE KINA	9.24e+02
857	5	5.0	949	4	Q9V4E8	KIAA0529 PROTEIN (FRAG	9.24e+02	930	5	5.0	1309	5	Q17582	C09H6.1 PROTEIN.	9.24e+02
858	5	5.0	949	10	Q41524	SINGLE-SUBUNIT RNA POL	9.24e+02	931	5	5.0	1312	5	Q44757	T12F5.4 PROTEIN.	9.24e+02
859	5	5.0	950	13	Q93508	PARAXIAL PROTOCADHERIN	9.24e+02	932	5	5.0	1339	5	Q26048	BETA-1,3-D-GLUCAN BIND	9.24e+02
860	5	5.0	951	2	Q68078	ICE NUCLEAR PROTEIN	9.24e+02	933	5	5.0	1345	14	Q9WT16	MAJOR CAPSID PROTEIN.	9.24e+02
861	5	5.0	954	10	Q23463	PUTATIVE OUTER MEMBRAN	9.24e+02	934	5	5.0	1371	4	Q94966	KIAA0891 PROTEIN (FRAG	9.24e+02
862	5	5.0	960	5	Q93137	SIMILARITY TO EXTENSIN	9.24e+02	935	5	5.0	1383	5	Q77086	GUANINE NUCLEOTIDE EXC	9.24e+02
863	5	5.0	961	10	Q65230	REVERSE TRANSCRIPTASE.	9.24e+02	936	5	5.0	1394	5	Q01787	SIMILARITY TO AN AMP-B	9.24e+02
864	5	5.0	961	14	Q65661	F7N22.14 PROTEIN.	9.24e+02	937	5	5.0	1415	5	Q94155	UNC-40 (T19B4.6 PROTEI	9.24e+02
865	5	5.0	963	10	Q9XE96	1A PROTEIN.	9.24e+02	938	5	5.0	1418	5	Q01837	SIMILARITY TO THE CATY	9.24e+02
866	5	5.0	964	5	Q10461	HYPOTHETICAL 106.3 KD	9.24e+02	939	5	5.0	1434	2	Q9X7H1	APP PROTEIN.	9.24e+02
867	5	5.0	964	2	Q84877	HYPOTHETICAL 106.7 KD	9.24e+02	940	5	5.0	1438	2	Q9Y2D6	KIAA0921 PROTEIN (FRAG	9.24e+02
868	5	5.0	976	5	Q19128	PUTATIVE OUTER MEMBRAN	9.24e+02	941	5	5.0	1438	5	Q96221	WEB-1 ORTHOLOG.. WD40.	9.24e+02
869	5	5.0	981	4	Q9V5B5	UBIQUITIN-SPECIFIC PRO	9.24e+02	942	5	5.0	1457	14	Q9WBO4	RNA-DEPENDENT RNA POLY	9.24e+02
870	5	5.0	982	3	Q74773	OSMIDIT F02G3.	9.24e+02	943	5	5.0	1457	14	Q9WJB3	RNA DEPENDENT RNA POLY	9.24e+02
871	5	5.0	984	9	Q80102	MSH2 (DNA REPAIR PROTE	9.24e+02	944	5	5.0	1463	14	Q9YN01	ORF1B POLYPROTEIN (FRA	9.24e+02
872	5	5.0	987	6	Q18966	ENDO-N-ACETYLNEURAMINI	9.24e+02	945	5	5.0	1471	5	Q18245	C27B7.7 PROTEIN.	9.24e+02
873	5	5.0	988	5	Q22317	EAG CHANNEL.	9.24e+02	946	5	5.0	1482	11	Q62684	NDAR2B GLUTAMATE RECU	9.24e+02
874	5	5.0	991	14	Q9VJS1	T07F10.1 PROTEIN.	9.24e+02	947	5	5.0	1507	11	Q63372	NEUREXIN I-ALPHA PRECU	9.24e+02
875	5	5.0	992	14	Q90706	1A PROTEIN.	9.24e+02	948	5	5.0	1525	5	Q94137	MULTIDRUG RESISTANCE R	9.24e+02
876	5	5.0	1002	14	Q9YN55	HELICASE.	9.24e+02	949	5	5.0	1526	11	Q55078	DNA TOPOISOMERASE II A	9.24e+02
877	5	5.0	1010	4	Q9S636	OUTER CAPSID PROTEIN V	9.24e+02	950	5	5.0	1526	11	Q55079	DNA TOPOISOMERASE II A	9.24e+02
878	5	5.0	1011	5	Q24273	MYELOID/LYMPHOID LEUK	9.24e+02	951	5	5.0	1537	13	Q92072	MODIFICATION METHYLASE	9.24e+02
879	5	5.0	1013	4	Q43897	NEUROMUSCULIN.	9.24e+02	952	5	5.0	1539	5	Q19611	SIMILARITY TO PUTATIVE	9.24e+02
880	5	5.0	1013	11	Q62381	TOLLOID-LIKE PROTEIN.	9.24e+02	953	5	5.0	1549	5	Q20060	F35G12.8 PROTEIN.	9.24e+02
881	5	5.0	1014	4	Q00406	TOLLOID-LIKE (MAMMALIA	9.24e+02	954	5	5.0	1581	4	Q92614	MYELOBLAST KIAA0216.	9.24e+02
882	5	5.0	1016	4	Q92585	G-PROTEIN-COUPLED RECE	9.24e+02	955	5	5.0	1581	2	Q92614	MYELOBLAST KIAA0216.	9.24e+02
883	5	5.0	1020	10	Q92VTV	MYELOBLAST KIAA0200.	9.24e+02	956	5	5.0	1581	2	Q92614	HYPOTHETICAL 181.4 KD	9.24e+02
884	5	5.0	1026	10	Q49529	F15K9.2 PROTEIN.	9.24e+02	957	5	5.0	1604	3	Q14148	HYPOTHETICAL 183.1 KD	9.24e+02
885	5	5.0	1029	14	Q9VXQ0	PREDICTED PROTEIN.	9.24e+02	958	5	5.0	1614	11	Q88883	LOW-DENSITY LIPOPROTEI	9.24e+02
886	5	5.0	1034	3	Q9V7E9	MUCIN-LIKE PROTEIN.	9.24e+02	959	5	5.0	1687	11	Q9WUF6	TUBEROUS SCLEROSIS 2 P	9.24e+02
887	5	5.0	1034	5	Q17117	FLO1P-RELATED LECTIN E	9.24e+02	960	5	5.0	1703	11	Q92019	COLLAGEN ALPHA3(VI) PR	9.24e+02
888	5	5.0	1038	5	Q61199	M51.4 PROTEIN.	9.24e+02	961	5	5.0	1706	14	Q56250	RNA POLYMERASE.	9.24e+02
889	5	5.0	1054	4	Q94887	T22B11.5 PROTEIN.	9.24e+02	962	5	5.0	1707	14	Q96806	PUTATIVE REPLICASE.	9.24e+02
890	5	5.0	1058	13	Q91480	KIAA0793 PROTEIN.	9.24e+02	963	5	5.0	1732	2	Q52050	LYSINE SPECIFIC CYSTEI	9.24e+02
891	5	5.0	1061	2	P73998	ACRIFLOPROTEIN B (FRAG	9.24e+02	964	5	5.0	1740	5	Q23891	ORF1740.	9.24e+02
892	5	5.0	1065	2	P71486	EMBR.	9.24e+02	965	5	5.0	1767	5	Q19346	F11C1.5 PROTEIN.	9.24e+02
893	5	5.0	1070	4	Q94938	KIAA0856 PROTEIN (FRAG	9.24e+02	966	5	5.0	1919	3	Q42998	HYPOTHETICAL 217.7 KD	9.24e+02
894	5	5.0	1082	14	Q9WT34	U30 PROTEIN.	9.24e+02	967	5	5.0	1976	6	Q27991	NONMUSCLE MYOSIN HEAVY	9.24e+02
895	5	5.0	1094	4	Q15032	KIAA0315.	9.24e+02	968	5	5.0	2098	5	Q25757	CTRP.	9.24e+02
896	5	5.0	1095	11	Q35867	NEURABIN.	9.24e+02	969	5	5.0	2134	14	Q9YLS4	AEV POLYPROTEIN.	9.24e+02
											2153	14	Q89709	VIRAL RNA POLYMERASE (9.24e+02

970 5 5.0 2204 14 Q9WHH6 LARGE PROTEIN. 9.24e+02
 971 5 5.0 2215 5 Q22465 COSMID T13H2. 9.24e+02
 972 5 5.0 2274 11 Q921K7 APC2 PROTEIN. 9.24e+02
 973 5 5.0 2282 11 Q61479 DNA BINDING PROTEIN RC 9.24e+02
 974 5 5.0 2314 11 Q9KVC7 A-KINASE ANCHOR PROTEI 9.24e+02
 975 5 5.0 2380 5 Q9G266 HYPOTHETICAL 283.6 KD 9.24e+02
 976 5 5.0 2460 11 Q64512 PROTEIN-TYROSINE PHOSP 9.24e+02
 977 5 5.0 2480 10 Q92PY3 F13A10.9 PROTEIN. 9.24e+02
 978 5 5.0 2488 5 Q61528 GUANINE NUCLEOTIDE EXC 9.24e+02
 979 5 5.0 2614 5 Q97054 TALIN HOMOLOGUE. 9.24e+02
 980 5 5.0 2627 4 Q95973 TELOMERASE-ASSOCIATED 9.24e+02
 981 5 5.0 2629 11 Q08653 TELOMERASE PROTEIN COM 9.24e+02
 982 5 5.0 2858 14 Q9WCE9 POLYPROTEIN. 9.24e+02
 983 5 5.0 2872 11 Q9WUH8 FIBRILLIN-1. 9.24e+02
 984 5 5.0 2948 5 Q93785 F54B4.1 PROTEIN. 9.24e+02
 985 5 5.0 3015 14 Q9WPH5 POLYPROTEIN. 9.24e+02
 986 5 5.0 3016 2 P73590 HYPOTHETICAL 311.5 KD 9.24e+02
 987 5 5.0 3064 14 Q9WSX7 UL36 PROTEIN. 9.24e+02
 988 5 5.0 3085 4 Q00183 BRCA2 (FRAGMENT). 9.24e+02
 989 5 5.0 3300 2 Q06304 HYPOTHETICAL 327.0 KD 9.24e+02
 990 5 5.0 3394 4 Q9Y6V0 WUGSC:H.DJ0784G16.1 PR 9.24e+02
 991 5 5.0 3418 4 Q13879 BRCA2 GENE EXON 2 (AND 9.24e+02
 992 5 5.0 3419 11 Q55147 UTROPHIN. 9.24e+02
 993 5 5.0 3582 2 Q66069 LICHENYSIN SYNTHETASE 9.24e+02
 994 5 5.0 3848 5 Q76737 TIPIC. 9.24e+02
 995 5 5.0 3898 14 Q09710 POLYPROTEIN. 9.24e+02
 996 5 5.0 3972 2 P73139 HYPOTHETICAL 418.3 KD 9.24e+02
 997 5 5.0 4005 4 Q13744 ALL-1 PROTEIN. 9.24e+02
 998 5 5.0 4017 14 Q88508 (PURDUE-115). 9.24e+02
 999 5 5.0 4152 2 Q9ZHL3 LARGE SUPERNATANT PROT 9.24e+02
 1000 5 5.0 7829 5 Q18559 SIMILAR TO POLYKETIDE 9.24e+02

ALIGNMENTS

RESULT 1
 ID 077088 PRELIMINARY; PRT; 994 AA.
 AC 077088;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
 DE DORSAL B.
 CN DL.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN [1]
 RC SEQUENCE FROM N.A.
 RA STRAIN-OREGON R;
 RL GROSS I., GEORGE P., OERTEL-BUCHHEIT P., SCHNARR M., REICHHART J.-M.;
 RT "Dorsal B, a splice variant of the Drosophila factor Dorsal, is a
 RT novel Rel/NF-kB transcription factor."
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF053614; AAC35296.1; -.
 DR HSP; P19838; INFI.
 DR PROSITE; PS01204; REL; 1.
 DR PFAM; PF00554; RHD; 1.
 DR PRINTS; PR00057; NFKBTNSCPFCT.
 SQ SEQUENCE 994 AA; 111523 MW; C0F47A7E CRC32;

Query Match 7.9%; Score 8; DB 5; Length 994;
 Best Local Similarity 100.0%; Pred. No. 1.18e-03;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 SSIDNSV 188
 Qy 32 SSIDNSV 39
 |||||

RESULT 2
 ID Q48425 PRELIMINARY; PRT; 100 AA.
 AC Q48425;

DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE HYPOTHETICAL PROTEIN (FRAGMENT).
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 RN [1]
 RC SEQUENCE FROM N.A.
 RA STRAIN-ATCC 25955;
 RL WILLARD B.L.;
 RL Thesis (1994), Chemical Engineering, University of Wisconsin-Madison,
 RL USA.
 RN [2]
 RC SEQUENCE FROM N.A.
 RA STRAIN-ATCC 25955;
 RC SKRALY F.A., WILLARD B.L., CAMERON D.C.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U30903; AAA74263.1; -.
 DR PFAM; PF00158; sigma54; 1.
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 100 AA; 11155 MW; 8B32A9F2 CRC32;

Query Match 6.9%; Score 7; DB 2; Length 100;
 Best Local Similarity 100.0%; Pred. No. 1.86e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 LNSVIEH 8
 Qy 36 LNSVIEH 42
 |||||

RESULT 3
 ID 005125 PRELIMINARY; PRT; 241 AA.
 AC 005125;
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
 DE MOLYBDENUM-BINDING SUBUNIT OF ABC-TRANSPORT SYSTEM PRECURSOR.
 CN MODA.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 RN [1]
 RC SEQUENCE FROM N.A.
 RA STRAIN-H37RV;
 RA LAQUEYRIERE A.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X99258; CAA67642.1; -.
 KW Signal.
 FT SIGNAL
 FT CHAIN
 SQ SEQUENCE 241 AA; 25286 MW; EE3621C1 CRC32;

Query Match 6.9%; Score 7; DB 2; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.86e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 AGSSELA 60
 Qy 64 AGSSELA 70
 |||||

RESULT 4
 ID P95157 PRELIMINARY; PRT; 261 AA.
 AC P95157;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
 DE HYPOTHETICAL 26.5 KD PROTEIN.
 CN MTCY359.16C.
 OS Mycobacterium tuberculosis.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA BROWN D., CHURCHER C.M.;
 RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA COLE S.T., BARRELL B.G., RAJANDREAM M.A.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE; 96181548.
 RA PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
 RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
 RA COLE S.T.;
 RL "An integrated map of the genome of the tubercle bacillus,
 RL Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
 RL leprae.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:3132-3137(1996).
 DR EMBL; 283859; CAB06130.1; -.
 DR HSSP; P37329; IAMF.
 KW Hypothetical protein.
 SQ SEQUENCE 261 AA; 26576 MW; FC5F6A79 CRC32;
 Query Match 6.9%; Score 7; DB 2; Length 261;
 Best Local Similarity 100.0%; Pred. No. 1.86e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 74 AGSSELA 80
 QY 64 AGSSELA 70
 RESULT 5
 ID Q20995 PRELIMINARY; PRT; 263 AA.
 AC Q20995;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE COSMID F5864.
 GN F5864.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 C Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE; 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPESEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MOSTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RL "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RL elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA DU Z., LEIMBAC D.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;

RA WATERSTON R.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA WATERSTON R.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U50309; AAB37061.1; -.
 DR PFAM; PF01461; 7tm_4; 1.
 SQ SEQUENCE 263 AA; 30016 MW; 7C4EFE67 CRC32;
 Query Match 6.9%; Score 7; DB 5; Length 263;
 Best Local Similarity 100.0%; Pred. No. 1.86e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 32 CRNTOLA 38
 QY 58 CRNTOLA 64
 RESULT 6
 ID Q41176 PRELIMINARY; PRT; 285 AA.
 AC Q41176;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE RIBOSOME-INACTIVATING PROTEIN-RELATED PROTEIN (FRAGMENT).
 OS Luffa cylindrica (Smooth loofah) (Sponge gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae;
 OC Luffa.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92338358.
 RA Li B.Y., RAMAKRISHNAN S.;
 RL "Cloning and expression of a Luffa ribosome-inactivating protein-
 RL related protein.";
 RL Targeted Diagn. Ther. 7:223-233(1992).
 DR EMBL; S40718; AAB22587.1; -.
 DR HSSP; P04475; LBPR.
 DR MENDEL; 15477; Lufcy; 146; 15477.
 DR PFAM; PF00012; HSP70; 1.
 FT NON_TER 1
 SQ SEQUENCE 285 AA; 30591 MW; DBFD38FC CRC32;
 Query Match 6.9%; Score 7; DB 10; Length 285;
 Best Local Similarity 100.0%; Pred. No. 1.86e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 21 AIOGSVL 27
 QY 12 AIOGSVL 18
 RESULT 7
 ID Q39254 PRELIMINARY; PRT; 399 AA.
 AC Q39254;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE LOW AFFINITY CALCIUM ANTI-PORTER CAX2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 OC Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RA HIRSCHI K.D., ZHEN R., CUNNINGHAM K.W., REA P.A., FINK G.R.;
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(0).
 DR EMBL; U57412; AAB05914.1; -.

DR MENDEL; 6872; Arath.1296;6872.
SQ SEQUENCE 399 AA; 43630 MW; 98395EE0 CRC32;

Query Match 6.9%; Score 7; DB 10; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.86e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 185 AGSELA 191
Qy 64 AGSELA 70
|||||||

RESULT 8 PRELIMINARY; PRT; 402 AA.
ID Q9LJ6 AC Q9LJ6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE POLYNUCLEOTIDE ADENYLITRANSFERASE.
GN PCNB.
OS Helicobacter pylori J99.
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J99;
RX MEDLINE; 99120557.
RA ALM R.A., LING L.-S.L., MOIR D.T., KING B.L., BROWN E.D., DOIG P.C.,
RA SMITH D.R., NOONAN B., GUILD B.C., DEJONGE B.L., CARMEL G.,
RA TUMMINO P.J., CARUSO A., URIA-NICKELSEN M., MILLS D.M., IVES C.,
RA GIBSON R., MERBERG D., MILLS S.D., JIANG Q., TAYLOR D.E., VOVIS G.F.,
RA TRUST T.J.;
RT "Genomic-sequence comparison of two unrelated isolates of the human
gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
DR EMBL; AE001491; AAD06174.1; -;
SQ SEQUENCE 402 AA; 46425 MW; F4369E21 CRC32;

Query Match 6.9%; Score 7; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.86e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 364 LNSVIEN 370
Qy 36 LNSVIEN 42
|||||||

RESULT 9 PRELIMINARY; PRT; 440 AA.
ID Q92KA2 AC Q92KA2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE ADENYLOSUCCINATE LYASE.
GN PURB.
OS Helicobacter pylori J99.
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J99;
RX MEDLINE; 99120557.
RA ALM R.A., LING L.-S.L., MOIR D.T., KING B.L., BROWN E.D., DOIG P.C.,
RA SMITH D.R., NOONAN B., GUILD B.C., DEJONGE B.L., CARMEL G.,
RA TUMMINO P.J., CARUSO A., URIA-NICKELSEN M., MILLS D.M., IVES C.,
RA GIBSON R., MERBERG D., MILLS S.D., JIANG Q., TAYLOR D.E., VOVIS G.F.,
RA TRUST T.J.;
RT "Genomic-sequence comparison of two unrelated isolates of the human
gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
DR EMBL; AE001531; AAD06609.1; -;
DR PROSITE; PS00163; FUMARATE LYASES; 1.
SQ SEQUENCE 440 AA; 49667 MW; 07B43099 CRC32;

Query Match 6.9%; Score 7; DB 2; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.86e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 327 LNSVIEN 333
Qy 36 LNSVIEN 42
|||||||

RESULT 10 PRELIMINARY; PRT; 465 AA.
ID Q9YVR4 AC Q9YVR4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE ORF MSV179 PUTATIVE METALLOPROTEASE, SIMILAR TO MUS MUSCULUS
DE GB:L36244.
GN MSV179.
OS Melanoplus sanguinipes entomopoxvirus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OC Entomopoxvirus B.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TUCSON;
RX MEDLINE; 99102612.
RA AFONSO C.L., TULMAN E.R., LU Z., OMA E., KUTISH G.F., ROCK D.L.;
RL "The genome of Melanoplus sanguinipes entomopoxvirus.";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TUCSON;
RA AFONSO C.L., TULMAN E.R., LU Z., OMA E., KUTISH G.F., ROCK D.L.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF063866; AAC97771.1; -;
KW Protease; Metalloprotease.
SQ SEQUENCE 465 AA; 54288 MW; 3171CDA6 CRC32;

Query Match 6.9%; Score 7; DB 14; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.86e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 192 IDLNSVI 198
Qy 34 IDLNSVI 40
|||||||

RESULT 11 PRELIMINARY; PRT; 606 AA.
ID Q59675 AC Q59675;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE ENDO-BETA-1,4-XYLANASE PRECURSOR (EC 3.2.1.8)
DE (ENDO-1,4-BETA-XYLANASE) (1,4-BETA-D-XYLAN XYLANOHYDROLASE).
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
OC Pseudomonas.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CELLULOSA;
RX MEDLINE; 96077124.
RA MILLWARD-SADLER S.J., DAVIDSON K., HAZLEWOOD G.P., BLACK G.W.,
RA GILBERT H.J., CLARKE J.H.;
RT "Novel cellulose-binding domains, NodB homologues and conserved
modular architecture in xylanases from the aerobic soil bacteria
Pseudomonas fluorescens subsp. cellulosa and Cellvibrio mixtus.";
RL Biochem. J. 312:39-48(1995).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
LINKAGES IN XYLANS.
DR EMBL; Z48928; CAA8764.1; -;
DR HSSP; P14768; ICLX.
DR PFAM; PF00331; Glyco_hydro_10; 1.

DR PRINTS: PR00134; GLHYDRASE10.
 KW Signal: Xylan degradation; Hydrolase; Glycosidase.
 FT SIGNAL 1 19 POTENTIAL.
 CHAIN 20 606
 SQ SEQUENCE 606 AA; 64841 MW; 07E3E2F2 CRC32;

Query Match 6.9%; Score 7; DB 2; Length 606;
 Best Local Similarity 100.0%; Pred. No. 1.86e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 184 LAGSSEL 190
 |||||
 QY 63 LAGSSEL 69

RESULT 12
 ID Q92WD9 PRELIMINARY; PRT; 938 AA.

AC Q92WD9;
 DT 01-MAY-1999 (TRENBLrel. 10, Created)
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
 DE F20N2.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 OC Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SHINN P., BUEHLER E., DEWAR K., DUNN P., FENG J., KIM C., WALKER M.,
 RA CONWAY A.B., CONWAY A.R., KURTZ D., OJI O., SHEN Y.K., TORIUMI M.,
 RA VYOTSKAIA V., YU G., DAVIS R.W., FEDERSPIEL N.A., THEOLOGIS A.,
 RA ECKER J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC F20N2";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC002328; AAC03063.1; --
 SQ SEQUENCE 938 AA; 103288 MW; EE7A6D4A CRC32;

Query Match 6.9%; Score 7; DB 10; Length 938;
 Best Local Similarity 100.0%; Pred. No. 1.86e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 254 AGSSELA 260
 |||||
 QY 64 AGSSELA 70

RESULT 13
 ID O89119 PRELIMINARY; PRT; 1115 AA.

AC O89119;
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
 DE PER3 (FRAGMENT).
 GN PER3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TAKUMI T., TAGUCHI K., MIYAKE S., SAKAKIDA Y., TAKASHIMA N.,
 RA MATSUBARA C., MAEBAYASHI Y., OKUMURA K., TAKEKIDA S., YAMAMOTO S.,
 RA YAGITA K., YAN L., YOUNG M.W., OKAMURA H.;
 RT "A light independent oscillatory gene mPer3 in mouse SCN and OVLT";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98372739.
 RA TAKUMI T., TAGUCHI K., MIYAKE S., SAKAKIDA Y., TAKASHIMA N.,
 RA MATSUBARA C., MAEBAYASHI Y., OKUMURA K., TAKEKIDA S., YAMAMOTO S.,
 RA YAGITA K., YAN L., YOUNG M.W., OKAMURA H.;
 RT "A light-independent oscillatory gene mPer3 in mouse SCN and OVLT";
 RL EMBO J. 17:4753-4759(1998).

DR EMBL; AJ007377; CAA07484.1; --
 DR EMBL; AB013605; BAA33465.1; --
 FT NON_TER 1115 1115
 SQ SEQUENCE 1115 AA; 121041 MW; D894816F CRC32;

Query Match 6.9%; Score 7; DB 11; Length 1115;
 Best Local Similarity 100.0%; Pred. No. 1.86e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 863 AGSSELA 869
 |||||
 QY 64 AGSSELA 70

RESULT 14
 ID Q92603 PRELIMINARY; PRT; 1152 AA.

AC Q92603;
 DT 01-FEB-1997 (TRENBLrel. 02, Created)
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
 DE KIAA0204 PROTEIN.
 GN KIAA0204.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97191544.
 RA NAGASE T., SEKI N., ISHIKAWA K., OHIRA M., KAWARAYASI Y., OHARA O.,
 RA TANAKA A., KOTANI H., MIYAJIMA N., NOMURA N.;
 RT "Prediction of the coding sequences of unidentified human genes. VI.
 RT The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by
 RT analysis of cDNA clones from cell line KG-1 and brain.";
 RL DNA Res. 3:321-329(1996).
 DR EMBL; D86959; BAA13195.1; --
 DR PFAM; PF00069; pkinase; 1.
 SQ SEQUENCE 1152 AA; 132796 MW; 4053FC00 CRC32;

Query Match 6.9%; Score 7; DB 4; Length 1152;
 Best Local Similarity 100.0%; Pred. No. 1.86e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 758 TSSIDLN 764
 |||||
 QY 31 TSSIDLN 37

RESULT 15
 ID O00211 PRELIMINARY; PRT; 1204 AA.

AC O00211;
 DT 01-JUL-1997 (TRENBLrel. 04, Created)
 DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
 DE HSLK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA YAMADA E., KAMEDA Y., ITOH S., KOHAMA Y., YAMAMOTO H., TSUJIKAWA K.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB002804; BAA19655.1; --
 DR PFAM; PF00069; pkinase; 1.
 SQ SEQUENCE 1204 AA; 138995 MW; 7486531D CRC32;

Query Match 6.9%; Score 7; DB 4; Length 1204;
 Best Local Similarity 100.0%; Pred. No. 1.86e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 758 TSSIDLN 764
 |||||
 QY 31 TSSIDLN 37

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RESULT 16
ID O85619 PRELIMINARY; PRT; 61 AA.
AC O85619;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE L0012.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-EDL933;
RX MEDLINE; 98339885.
RA PERNA N.T., MAYHEW G.F., POSFAI G., ELLIOTT S., DONNENBERG M.S.,
RA KAPER J.B., BLATTNER F.R.;
RT "Molecular evolution of a pathogenicity island from enterohemorrhagic
RT Escherichia coli O157:H7.";
RL Infect. Immun. 66:3810-3817(1998).
EMBL; AF071034; AAC31491.1; -.
SEQUENCE 61 AA; 7286 MW; D92B85CF CRC32;

Query Match 5.9%; Score 6; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 43 INLDDH 48
QY 85 INLDDH 90

RESULT 17
ID O92440 PRELIMINARY; PRT; 85 AA.
AC O92440;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE ACNPNV ORF76.
OS Bombyx mori nuclear polyhedrosis virus (BmNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-T3;
RX MEDLINE; 97329351.
RA KAWITA S.G., MAEDA S.;
RT "Sequencing of the putative DNA helicase-encoding gene of the Bombyx
RT mori nuclear polyhedrosis virus and fine-mapping of a region involved
RT in host range expansion.";
RL Gene 190:173-179(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-T3;
RA GOMI S., MAJIMA K., MAEDA S.;
RT "Sequence analysis of the genome of Bombyx mori
RT nucleopolyhedrovirus.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; L33180; AAC63748.1; -.
SEQUENCE 85 AA; 9582 MW; 5361427C CRC32;

Query Match 5.9%; Score 6; DB 14; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 80 NTSSID 85
QY 30 NTSSID 35

RESULT 18
ID O57168 PRELIMINARY; PRT; 91 AA.
AC O57168;

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DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
DE FRAGMENT OF 28K VIRULENCE FACTOR.
GN MYA007R.
OS Vaccinia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ANKARA;
RA ANTOINE G., SCHEIFLINGER F., FALKNER F.G., DORNER F.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U94848; AAB96483.1; -.
SEQUENCE 91 AA; 10637 MW; AA9D4906 CRC32;

Query Match 5.9%; Score 6; DB 14; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 NTSSID 14
QY 30 NTSSID 35

RESULT 19
ID O23930 PRELIMINARY; PRT; 92 AA.
AC O23930;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4.1.1.31) (FRAGMENT).
GN PPC1 OR PPCB.
OS Flaveria pringlei.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Asteridae; euasterids II; Asterales; Asteraceae;
OC Asteroideae; Heleniaceae; Flaveria.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LEAF;
RX MEDLINE; 97369366.
RA ERNST K.A., WESTHOFF P.;
RT "The phosphoenolpyruvate carboxylase (ppc) gene family of Flaveria
RT trinervia (C4) and F. pringlei (C3): molecular characterization and
RT expression analysis of the ppcB and ppcC genes.";
RL Plant Mol. Biol. 34:427-443(1997).
CC -1- CATALYTIC ACTIVITY: PHOSPHATE + OXALOACETATE = H(2)O +
CC PHOSPHOENOLPYRUVATE + CO(2).
DR EMBL; Z71977; CAA96509.1; -.
DR MENDEL; 24103; FlapR:Ppc1;24103.
DR PFAM; PF00311; PEPcase; 1.
KW Pyruvate; Lyase.
FT NON_TER 92
SQ SEQUENCE 92 AA; 10258 MW; 988E3186 CRC32;

Query Match 5.9%; Score 6; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 75 GSVLTS 80
QY 15 GSVLTS 20

RESULT 20
ID Q49442 PRELIMINARY; PRT; 94 AA.
AC Q49442;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
DE UNCERTAIN (FRAGMENT).
OS Mycoplasma genitalium.

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OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Mycoplasma.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-G-37;

RA PETERSON S.N., HU P., BOTT K.F., HUTCHISON C.A.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-G-37;

RA PETERSON S.N.;

RL Thesis (1992). Microbiology and Immunology,
 RL University of North Carolina Medical School, USA.

DR EMBL; 001738; AAD10348.1; -

FT NON_TER 94

SQ SEQUENCE 94 AA; 11001 MW; 832863C0 CRC32;

Query Match 5.9%; Score 6; DB 2; Length 94;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 40 NSVIEH 45

|||||

QY 37 NSVIEH 42

RESULT 21

ID O82254 PRELIMINARY; PRT; 103 AA.

AC O82254;

DT 01-NOV-1998 (TRENBLrel. 08, Created)

DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)

DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)

DE PUTATIVE GLUTAREDOXIN.

GN F17A22.26 OR T9J23.3.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC eudicotyledons; Magnoliophyta; eudicotyledons;

OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;

OC Arabidopsis.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-CV. COLUMBIA;

RA ROUNSLEY S.D., LIN X., KAUL S., SHEA T.P., FUJII C.Y., MASON T.M.,

RA SHEN M., RONNING C.M., FRASER C.M., SOMERVILLE C.R., VENTER J.C.;

RL "Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence.";

RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-CV. COLUMBIA;

RA LIN X., KAUL S., SHEA T.P., FUJII C.Y., SHEN M., VANAKEN S.E.,

RA BARNSTEAD M.E., MASON T.M., BOWMAN C.L., RONNING C.M., BENITO M.,

RA CARRERA A.J., CREASY T.H., BUELL C.R., TOWN C.D., NIERMAN W.C.,

RA FRASER C.M., VENTER J.C.;

RT "Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence.";

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC005309; AAC63641.1; -

DR EMBL; AC006072; AAD13692.1; -

DR MENDEL; 32853; Arath; 2723; 32853.

DR MENDEL; 35583; Arath; 2723; 35583.

SQ SEQUENCE 103 AA; 11261 MW; 9089B2A5 CRC32;

Query Match 5.9%; Score 6; DB 10; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 87 VDSGLK 92

|||||

QY 43 VDSGLK 48

RESULT 22

ID Q9YEB4 PRELIMINARY; PRT; 109 AA.

AC Q9YEB4;

DT 01-NOV-1999 (TRENBLrel. 12, Created)

DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)

DE 109AA LONG HYPOTHETICAL PROTEIN.

GN APE0660.

OS Aeropyrum pernix.

OC Archaea; Crenarchaeota; Aeropyrum.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-K1;

RX MEDLINE; 99310339.

RA KAWARABAYASI Y., HINO Y., HORIKAWA H., YAMAZAKI S., HAIKAWA Y.,

RA JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H.,

RA HOSOYAMA A., FUKUI S., NAGAI Y., NISHIJIMA K., NAKAZAWA H.,

RA TAKAMIYA M., MASUDA S., FUNAHASHI T., TANAKA T., KUDOH Y.,

RA YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA Y.,

RA NOMURA N., SAKO Y., KIKUCHI H.;

RT "Complete genome sequence of an aerobic hyper-thermophilic

RT crenarchaeon, Aeropyrum pernix K1.";

RL DNA Res. 6:83-101(1999).

DR EMBL; AP000060; BAA79632.1; -

SQ SEQUENCE 109 AA; 12078 MW; 6151914F CRC32;

Query Match 5.9%; Score 6; DB 1; Length 109;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 72 ENVDGS 77

|||||

QY 41 ENVDGS 46

RESULT 23

ID Q86610 PRELIMINARY; PRT; 110 AA.

AC Q86610;

DT 01-NOV-1996 (TRENBLrel. 01, Created)

DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)

DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)

DE BILF2-PUTATIVE GLYCOPROTEIN [PROMOTER] (FRAGMENT).

GN BILF2.

OS Human herpesvirus 4 (Epstein-Barr virus).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Gammaherpesvirinae; Lymphocryptovirus.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 93267769.

RA SMITH P.R., CAO Y., KARRAN L., JONES M.D., SNUDDEN D., GRIFFIN B.E.;

RT "Complex nature of the major viral polyadenylated transcripts in

RT Epstein-Barr virus-associated tumors.";

RL J. Virol. 67:3217-3225(1993).

DR EMBL; S61077; CAB31989.1; -

FT NON_TER 110

SQ SEQUENCE 110 AA; 11611 MW; 82005F0C CRC32;

Query Match 5.9%; Score 6; DB 14; Length 110;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 78 TNGGYN 83

|||||

QY 25 TNGGYN 30

RESULT 24

ID Q22483 PRELIMINARY; PRT; 139 AA.

AC Q22483;

DT 01-NOV-1996 (TRENBLrel. 01, Created)

DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)

DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)

DE COSMID T14B4.

GN T14B4.2.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE; 94150718;
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKIN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX FAVELLO T.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U50191; AAA91243.1; -;
SQ SEQUENCE 139 AA; 15778 MW; 4F1FC5D9 CRC32;

Query Match 5.9%; Score 6; DB 5; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 72 QQFVST 77
QY 78 QQFVST 83
|||||

RESULT 25
ID O15186 PRELIMINARY; PRT; 154 AA.
AC O15186;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE COLLA1 AND PDGFB FUSION TRANSCRIPT (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA O'BRIEN K.P.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA O'BRIEN K.P.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y08643; CAA6933.1; -;
DR EMBL; Y15920; CAA75880.1; -;
DR EMBL; Y15914; CAA75874.1; -;
DR HSSP; P01127; 1PDG.
DR PFAM; PF00341; PDGF; 1.
FT NON_TER 1 154
FT NON_TER 154 154
SQ SEQUENCE 154 AA; 16512 MW; 6DD0301B CRC32;

Query Match 5.9%; Score 6; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 120 AECKTR 125
QY 71 AECKTR 76
|||||

RESULT 26
ID O65096 PRELIMINARY; PRT; 156 AA.

Query Match 5.9%; Score 6; DB 10; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 14 TCYNSA 19
QY 7 TCYNSA 12
|||||

RESULT 27
ID Q9WVQ6 PRELIMINARY; PRT; 158 AA.
AC Q9WVQ6;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE PDGF B (FRAGMENT).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-APA; TISSUE-KIDNEY;
RA NISHIDA E.;
RT "APA hamsters PDGF B partial cDNA";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB028638; BAA78769.1; -;
DR PROSITE; PS00249; PDGF; 1.
FT NON_TER 1 158
FT NON_TER 158 158
SQ SEQUENCE 158 AA; 17608 MW; C4EB5CC3 CRC32;

Query Match 5.9%; Score 6; DB 11; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 79 AECKTR 84
QY 71 AECKTR 76
|||||

RESULT 28
ID O70699 PRELIMINARY; PRT; 163 AA.
AC O70699;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 08, Last annotation update)
DE HYPOTHETICAL 17.8 KD PROTEIN.
OS human Calicivirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Calicivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SAPORO-LIKE;
RX MEDLINE; 98336510.

AC O65096;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE ATAF1-LIKE PROTEIN (FRAGMENT).
GN SB29.
OS Picea mariana (Black spruce).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
OC Picea.
RN [1]
RP SEQUENCE FROM N.A.
RA PERRY D.J., BOUSQUET J.;
RL Genetics 0:0-0(1998).
DR EMBL; AF051749; AAC32166.1; -;
DR MENDEL; 28868; Picma; 3421; 28868.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 156 AA; 17489 MW; AIDA6728 CRC32;

Query Match 5.9%; Score 6; DB 10; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 14 TCYNSA 19
QY 7 TCYNSA 12
|||||

RESULT 27
ID Q9WVQ6 PRELIMINARY; PRT; 158 AA.
AC Q9WVQ6;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE PDGF B (FRAGMENT).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-APA; TISSUE-KIDNEY;
RA NISHIDA E.;
RT "APA hamsters PDGF B partial cDNA";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB028638; BAA78769.1; -;
DR PROSITE; PS00249; PDGF; 1.
FT NON_TER 1 158
FT NON_TER 158 158
SQ SEQUENCE 158 AA; 17608 MW; C4EB5CC3 CRC32;

Query Match 5.9%; Score 6; DB 11; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 79 AECKTR 84
QY 71 AECKTR 76
|||||

RESULT 28
ID O70699 PRELIMINARY; PRT; 163 AA.
AC O70699;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 08, Last annotation update)
DE HYPOTHETICAL 17.8 KD PROTEIN.
OS human Calicivirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Calicivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SAPORO-LIKE;
RX MEDLINE; 98336510.

RA JIANG X., CUBITT D.W., BERKE T., ZHONG W.M., DAI X.M., PICKERING L.K.,
 RA MATSON D.O.;
 RT "Saporo-like human caliciviruses are genetically and antigenically
 RT diverse.";
 RL Arch. Virol. 142:1813-1827(1997).
 DR EMBL; U95644; AAC40582.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 163 AA; 17837 MW; B9B5AE28 CRC32;

Query Match 5.9%; Score 6; DB 14; Length 163;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 87 LAGSSE 92
 QY 63 LAGSSE 68
 |||||

RESULT 29
 ID O09726 PRELIMINARY; PRT; 163 AA.
 AC O09726;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE HYPOTHETICAL 17.8 KD PROTEIN.
 OS human calicivirus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Calicivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PARKVILLE;
 RA LIU B.L., LAMBDEN P.R., CLARKE I.N., NOEL J.S., ANDO T.,
 RA HUMPHREY C.D., GROVES C., MONROE S.S.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U73124; AAB51209.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 163 AA; 17811 MW; 1D308499 CRC32;

Query Match 5.9%; Score 6; DB 14; Length 163;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 87 LAGSSE 92
 QY 63 LAGSSE 68
 |||||

RESULT 30
 ID O89074 PRELIMINARY; PRT; 164 AA.
 AC O89074;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE GUANINE NUCLEOTIDE EXCHANGE FACTOR LSC (FRAGMENT).
 GN LSC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=SPLEEN;
 RX MEDLINE; 99012997.
 RA CHU C.C., PAUL W.B.;
 RT "Expressed genes in interleukin-4 treated B cells identified by cDNA
 RT representational difference analysis.";
 RL Mol. Immunol. 35:487-502(1998).
 DR EMBL; U89421; AAC36527.1; -;
 FT NON_TER 1 1
 FT NON_TER 164 164
 SQ SEQUENCE 164 AA; 19062 MW; 933835E2 CRC32;

Query Match 5.9%; Score 6; DB 11; Length 164;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;

RA JIANG X., CUBITT D.W., BERKE T., ZHONG W.M., DAI X.M., PICKERING L.K.,
 RA MATSON D.O.;
 RT "Saporo-like human caliciviruses are genetically and antigenically
 RT diverse.";
 RL Arch. Virol. 142:1813-1827(1997).
 DR EMBL; U95644; AAC40582.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 163 AA; 17837 MW; B9B5AE28 CRC32;

Query Match 5.9%; Score 6; DB 14; Length 163;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 87 LAGSSE 92
 QY 63 LAGSSE 68
 |||||

RESULT 29
 ID O09726 PRELIMINARY; PRT; 163 AA.
 AC O09726;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE HYPOTHETICAL 17.8 KD PROTEIN.
 OS human calicivirus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Calicivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PARKVILLE;
 RA LIU B.L., LAMBDEN P.R., CLARKE I.N., NOEL J.S., ANDO T.,
 RA HUMPHREY C.D., GROVES C., MONROE S.S.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U73124; AAB51209.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 163 AA; 17811 MW; 1D308499 CRC32;

Query Match 5.9%; Score 6; DB 14; Length 163;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 87 LAGSSE 92
 QY 63 LAGSSE 68
 |||||

RESULT 30
 ID O89074 PRELIMINARY; PRT; 164 AA.
 AC O89074;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE GUANINE NUCLEOTIDE EXCHANGE FACTOR LSC (FRAGMENT).
 GN LSC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=SPLEEN;
 RX MEDLINE; 99012997.
 RA CHU C.C., PAUL W.B.;
 RT "Expressed genes in interleukin-4 treated B cells identified by cDNA
 RT representational difference analysis.";
 RL Mol. Immunol. 35:487-502(1998).
 DR EMBL; U89421; AAC36527.1; -;
 FT NON_TER 1 1
 FT NON_TER 164 164
 SQ SEQUENCE 164 AA; 19062 MW; 933835E2 CRC32;

Query Match 5.9%; Score 6; DB 11; Length 164;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 32 ELAAEC 37
 QY 68 ELAAEC 73
 |||||

RESULT 31
 ID Q9XZ63 PRELIMINARY; PRT; 172 AA.
 AC Q9XZ63;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE ARP-LIKE PROTEIN.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON R;
 RA GOO J.H., AHN Y., PARK O.K., PARK W.J.;
 RT "Selection of Drosophila genes encoding secreted and membrane
 RT proteins.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF132912; AAD32615.1; -;
 SQ SEQUENCE 172 AA; 19973 MW; 830F6C1C CRC32;

Query Match 5.9%; Score 6; DB 5; Length 172;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 IDLSNV 126
 QY 34 IDLSNV 39
 |||||

RESULT 32
 ID O11337 PRELIMINARY; PRT; 173 AA.
 AC O11337;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE CLONE B2-24B HOMOLOG OF VACCINIA H3L (B2-24B) (FRAGMENT).
 GN B2-24B.
 OS Molluscum contagiosum virus subtype 1 (MCV1).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Molluscipoxvirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MORATILLA M., AGROMAYOR M., NUNEZ A., FUNES J.M., VARAS A.J.,
 RA LOPEZ-ESTEBAN M., ESTEBAN M., MARTIN-GALLARDO A.;
 RL VIRUS Genes 0:0-0(0).
 DR EMBL; U86915; AAB57970.1; -;
 FT NON_TER 1 1
 FT NON_TER 173 173
 SQ SEQUENCE 173 AA; 18980 MW; 20C79577 CRC32;

Query Match 5.9%; Score 6; DB 14; Length 173;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 78 LAGSSE 83
 QY 63 LAGSSE 68
 |||||

RESULT 33
 ID P74001 PRELIMINARY; PRT; 178 AA.
 AC P74001;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)

DE HYPOTHETICAL 20.6 KD PROTEIN.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PCC6803;
 RA TABATA S.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PCC6803;
 RX MEDLINE: 97061201.
 RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
 RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
 RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
 RA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
 RA TABATA S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. II. Sequence determination of the
 entire genome and assignment of potential protein-coding regions.";
 RT DNA Res. 3:109-136(1996).
 RM EMBL: D90911; BAA18072.1; -.
 KN Hypothetical protein.
 SQ SEQUENCE 178 AA; 20608 MW; 73BB2CFA CRC32;
 Query Match 5.9%; Score 6; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 140 SSELAA 145
 QY 66 SSELAA 71
 RESULT 34
 ID 083736 PRELIMINARY; PRT; 180 AA.
 AC 083736;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DE PTS SYSTEM, NITROGEN REGULATORY IIA COMPONENT (PTSN-2).
 GN TP0755.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 98332770.
 RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
 RA DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
 RA SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
 RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
 RA MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
 RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
 RA VENTER J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 spirochete.";
 RT Science 281:375-388(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
 RA DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
 RA SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
 RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
 RA MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
 RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
 RA VENTER J.C.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE001247; AAC65722.1; -.
 DR HSSP: P31222; 1A6J.
 DR TIGR: TP0755; -.
 SQ SEQUENCE 180 AA; 20428 MW; 1A78EB52 CRC32;
 Query Match 5.9%; Score 6; DB 2; Length 180;

Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 69 SELAAE 74
 QY 67 SELAAE 72
 RESULT 35
 ID Q15354 PRELIMINARY; PRT; 185 AA.
 AC Q15354;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE C-SIS PROTO-ONCOGENE (FRAGMENT).
 DE C-SIS PROTO-ONCOGENE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-CHORIOCARCINOMA;
 RX MEDLINE: 95388493.
 RA DIRKS R.P.H., ONNEKINK C., JANSEN H.J., DE JONG A., BLOEMERS H.P.J.;
 RT "A novel human c-sis mRNA species is transcribed from a promoter in c-
 sis intron 1 and contains the code for an alternative PDGF B-like
 protein.";
 RT Nucleic Acids Res. 23:2815-2822(1995).
 RL EMBL: X83705; CAA58679.1; -.
 DR HSSP: P01127; 1PDG.
 DR PROSITE: PS00249; PDGF; 1.
 DR PFAM: PF00341; PDGF; 1.
 FT NON_TER 185 185
 SQ SEQUENCE 185 AA; 20774 MW; C5FAA883 CRC32;
 Query Match 5.9%; Score 6; DB 4; Length 185;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 80 AECKTR 85
 QY 71 AECKTR 76
 RESULT 36
 ID 027457 PRELIMINARY; PRT; 191 AA.
 AC 027457;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DE FUCULOSE-1-PHOSPHATE ALDOLASE.
 GN MTH1406.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
 OC Methanobacterium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DELTA H;
 RX MEDLINE: 98037514.
 RA SMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.,
 RA ALDREDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
 RA HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D.,
 RA SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
 RA JIWANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,
 RA MCDUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
 RA DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 J. Bacteriol. 179:7135-7155(1997).
 RL EMBL: AE000903; AAB85883.1; -.
 DR HSSP: P11550; 3FUA.
 DR PFAM: PF00596; Aldolase_II; 1.
 SQ SEQUENCE 191 AA; 20702 MW; BC8B78DC CRC32;

Query Match 5.9%; Score 6; DB 1; Length 191;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 134 ELAAEC 139
 QY 68 ELAAEC 73

RESULT 37
 ID Q65594 PRELIMINARY; PRT; 198 AA.
 AC Q65594;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
 DE W44D2.5 PROTEIN.
 GN VIF.
 OS Bovine immunodeficiency-like virus.
 OC Viruses; Retroviridae; Lentivirus.
 RN [1]
 RA NADIN-DAVIS S.A., CHANG S.C., ROTH J.A., CARPENTER S.;
 RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L04972; AAA42764.1; -;
 SQ SEQUENCE 198 AA; 22836 MW; C545A8B2 CRC32;

Query Match 5.9%; Score 6; DB 14; Length 198;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 141 SVLTST 146
 QY 16 SVLTST 21

RESULT 38
 ID Q65591 PRELIMINARY; PRT; 198 AA.
 AC Q65591;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
 DE VIF PROTEIN.
 GN VIF.
 OS Bovine immunodeficiency-like virus.
 OC Viruses; Retroviridae; Lentivirus.
 RN [1]
 RA NADIN-DAVIS S.A., CHANG S.C., ROTH J.A., CARPENTER S.;
 RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L04974; AAA42764.1; -;
 SQ SEQUENCE 198 AA; 22797 MW; F5621CAA CRC32;

Query Match 5.9%; Score 6; DB 14; Length 198;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 141 SVLTST 146
 QY 16 SVLTST 21

RESULT 39
 ID Q23155 PRELIMINARY; PRT; 208 AA.
 AC Q23155;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE W04D2.5 PROTEIN.
 GN W04D2.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]

RP SEQUENCE FROM N.A.
 RA LENNARD N.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94150718.
 RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M., COULSON A.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., FULTON L.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).
 DR EMBL; 275552; CAA99938.1; -;
 DR PFAM; PF00411; Ribosomal_S11; 1.
 SQ SEQUENCE 208 AA; 22586 MW; 79CBFB88 CRC32;

Query Match 5.9%; Score 6; DB 5; Length 208;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 71 NTSSID 76
 QY 30 NTSSID 35

RESULT 40
 ID Q29613 PRELIMINARY; PRT; 210 AA.
 AC Q29613;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE C-SIS ONCOGENE (PLATELET-DERIVED GROWTH FACTOR).
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87146463.
 RA VAN DEN OuwELAND A.M.W., VAN GRONINGEN J.J.M., SCHALKEN J.A.,
 RA VAN NECK H.W., BLOEMERS P.J., VAN DE VEN W.J.M.;
 RL "Genetic organization of the c-sis transcription unit.";
 RN Nucleic Acids Res. 15:959-970(1987).
 RN [2]
 RP SEQUENCE OF 1-21 FROM N.A.
 RX MEDLINE; 86120370.
 RA VAN DEN OuwELAND A.M.W., ROEBROEK A.J.M., SCHALKEN J.A.,
 RA CLAESSEN C.A., BLOEMERS H.P.J., VAN DE VEN W.J.M.;
 RL "Structure and nucleotide sequence of the 5' region of the human and
 RL feline c-sis proto-oncogenes.";
 RL Nucleic Acids Res. 14:765-778(1986).
 DR EMBL; X06297; CAA29623.1; -;
 DR EMBL; X06298; CAA29623.1; JOINED.
 DR EMBL; X06299; CAA29623.1; JOINED.
 DR EMBL; X06300; CAA29623.1; JOINED.
 DR EMBL; X06301; CAA29623.1; JOINED.
 DR EMBL; X06302; CAA29623.1; JOINED.
 DR EMBL; X03494; CAA27210.1; -;
 DR EMBL; M25358; AAA30817.1; -;
 DR EMBL; M25356; AAA30817.1; JOINED.
 DR EMBL; M25357; AAA30817.1; JOINED.
 DR EMBL; M25353; AAA30817.1; JOINED.
 DR EMBL; M25354; AAA30817.1; JOINED.
 DR EMBL; M25355; AAA30817.1; JOINED.
 DR HSSP; P01127; IPDG.
 DR PROSITE; PS00249; PDGF; 1.
 DR PFAM; PF00341; PDGF; 1.

DR PRINTS: PR00438; GFCYSKNOT.
SQ SEQUENCE 210 AA; 23649 MW; 1579ED72 CRC32;

Query Match 5.9%; Score 6; DB 6; Length 210;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 99 AECCTR 104
|||||
QY 71 AECCTR 76

RESULT 41
ID Q19865 PRELIMINARY; PRT; 219 AA.
AC Q19865;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JAN-1999 (TRENBLrel. 09, Last annotation update)
DE F28C6.5 PROTEIN.
GN F28C6.5.
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
[1]
RN BURTON J.;
RP SEQUENCE FROM N.A.
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON F., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPESEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THLERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL; Z68315; CAA92671.1; -.
SQ SEQUENCE 219 AA; 24585 MW; 97C9A806 CRC32;

Query Match 5.9%; Score 6; DB 5; Length 219;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 113 SELAAE 118
|||||
QY 67 SELAAE 72

RESULT 42
ID P96667 PRELIMINARY; PRT; 219 AA.
AC P96667;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE YDEJ PROTEIN.
GN YDEJ.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-168;
RX MEDLINE; 98000887.
RA BELOIN C., AYORA S., EXLEY R., HIRSCHBEIN L., OGASAWARA N.,
RA KASAHARA Y., ALONSO J.C., LE HEGARAT F.;
RT "Characterization of an lrp-like (lrpC) gene from Bacillus subtilis.";

Mol. Gen. Genet. 256:63-71(1997).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN-168;
RX MEDLINE; 98044033.
RA KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA BORRIS R., BOURSIER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
RA CHOI S.K., CODANT J.J., CONNERTON I.F., CUMINGS N.J., DANIEL R.A.,
RA DENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMMERSON P.T.,
RA ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D.,
RA FRITZ C., FUJITA M., FUJITA Y., FUMA S., GALIZZI A., GALLERON N.,
RA GHIM S.Y., GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G.,
RA GUISEPPI G., GUY B.J., HAGA K., HAIRCH J., HARWOOD C.R., HENAUT A.,
RA HILBERT H., HOLSAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,
RA JORIS B., KARAMATA D., KASAHARA Y., KLAERR-BLANCHARD M., KLEIN C.,
RA KOBAYASHI Y., KOETTER P., KONINGSTEIN G., KROGH S., KUMANO M.,
RA KURITA K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
RA LEE S.M., LEVINE A., LIU H., MASUDA S., MAUEL C., MEDIGUE C.,
RA MEDINA N., MELLADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
RA NOONE D., O'REILLY M., OGAWA K., OGIWARA A., OUDEGA B., PARK S.H.,
RA PARO V., POHL T.M., PORTELELLA D., PORMOLLIK S., PRESCOTT A.M.,
RA PRESECAN E., PUJIC P., PURNELLE B., RAPOPORT G., REY M., REYNOLDS S.,
RA RIEGER M., RIVOLTA C., ROCHE E., ROCHE B., ROSE M., SADALE Y.,
RA SATO T., SCANLAN E., SCHLEICH S., SCHROETER R., SCOFFONE F.,
RA SEKIGUCHI J., SEKOWSKA A., SEROR S.J., SERROR P., SHIN B.S., SOLDI B.,
RA SOROKIN A., TACCONI E., TAKAGI T., TAKAHASHI H., TAKEMARU K.,
RA TAKEUCHI M., TAKAKOSHI A., TANAKA T., TERPSTRA P., TOGNONI A.,
RA TOSATO V., UCHIYAMA S., VANDENBOL M., VANNIER F., VASSAROTTI A.,
RA VIARI A., WAMBUIT R., WEDLER E., WEDLER H., WEITZENEGER T.,
RA WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K., YASUMOTO K., YATA K.,
RA YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RA KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB001488; BAA19357.1; -.
DR EMBL; Z99106; CAB12329.1; -.
SQ SEQUENCE 219 AA; 24355 MW; E4D588E4 CRC32;

Query Match 5.9%; Score 6; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 143 TQLAGS 148
|||||
QY 61 TQLAGS 66

RESULT 43
ID Q98708 PRELIMINARY; PRT; 225 AA.
AC Q98708;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE V-SIS TRANSFORMING PROTEIN P28.
OS Simian sarcoma virus.
OC Viruses; Retroviridae; Retroviridae; Mammalian type C retroviruses.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 82242320.
RA DEVARE S.G., REDDY P.E., LAW J.D., AARONSON S.A.;
RT "Nucleotide sequence analysis of the long terminal repeat of
RT integrated simian sarcoma virus: evolutionary relationship with other
RT mammalian retroviral long terminal repeats.";
RL J. Virol. 42:1108-1113(1982).
RN [2]
RP SEQUENCE FROM N.A.

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RX MEDLINE; 82247820.
RA DEVARE S.G., REDDY P.E., ROBBINS K.C., ANDERSEN P.R., TRONICK S.R.,
RT "Nucleotide sequence of the transforming gene of simian sarcoma
RL virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:3179-3182(1982).
RN [3]
RP SEQUENCE OF 1-36 FROM N.A.
RX MEDLINE; 83067415.
RA ROBBINS K.C., DEVARE S.G., REDDY P.E., AARONSON S.A.;
RT "In vivo identification of the transforming gene product of simian
RL sarcoma virus.";
RL Science 218:1131-1133(1982).
RN [4]
RP SEQUENCE OF 1-9 FROM N.A.
RX MEDLINE; 84106822.
RA DEVARE S.G., SHATZMAN A., ROBBINS K.C., ROSENBERG M., AARONSON S.A.;
RT "Expression of the PDGF-related transforming protein of simian sarcoma
RL virus in E. coli.";
RL Cell 36:43-49(1984).
DR EMBL; J02396; AAA46814.1; -.
DR HSSP; P01127; LPDG.
DR PFAM; PF00341; PDGF; 1.
SQ SEQUENCE 225 AA; 24347 MW; 41165581 CRC32;

Query Match 5.9%; Score 6; DB 14; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 80 ABEKTR 85
QY 71 ABEKTR 76

RESULT 44
ID Q02062 PRELIMINARY; PRT; 232 AA.
AC Q02062;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE CODED FOR BY C. ELEGANS CDNA CEESM67F.
GN F41C3.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RL MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIRRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RA CHISSOE S.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U23521; AAC46813.1; -.

SQ SEQUENCE 232 AA; 26687 MW; 3C5DE33B CRC32;

Query Match 5.9%; Score 6; DB 5; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 KFSQTC 151
QY 3 KFSQTC 8

RESULT 45
ID O49374 PRELIMINARY; PRT; 233 AA.
AC O49374;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE HYPOTHETICAL 25.6 KD PROTEIN.
GN F10N7.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RA BEVAN M., KOETTER P., HEMPEL S., ENTIAN K.-D., HOHEISEL J.,
RA MEWES H.W., MAYER K., SCHUELLER C.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU ARABIDOPSIS SEQUENCING PROJECT;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL021636; CAA16571.1; -.
DR MENDEL; 27479; Arath; 3375; 27479.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 25640 MW; 4C2537BB CRC32;

Query Match 5.9%; Score 6; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 211 SSELAA 216
QY 66 SSELAA 71

RESULT 46
ID O04392 PRELIMINARY; PRT; 240 AA.
AC O04392;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE ALBURNE RIBONUCLEASE (FRAGMENT).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
OC Poaceae; Hordeum.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-CV. HIMALAYA;
RA ROGERS J.C., ROGERS S.W.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF000939; AAB58718.1; -.
DR MENDEL; 14798; Horvu; 1285; 14798.
DR PROSITE; PS00530; RNASE_T2_1; 1.
DR PROSITE; PS00531; RNASE_T2_2; 1.
DR PFAM; PF00445; ribonuclease_T2; 1.
FT NON_TER 240 240
SQ SEQUENCE 240 AA; 26989 MW; 3CC14846 CRC32;

Query Match 5.9%; Score 6; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 65 ABEKTR 70
|||||
Qy 71 ABEKTR 76

RESULT 47
ID Q85318 PRELIMINARY; PRT; 241 AA.
AC Q85318;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE RING ZINC FINGER-CONTAINING PROTEIN, HOMOLOGUE OF VARIOLO D4.
GN P28.
OS Ectromelia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
RN [1]
RP SEQUENCE FROM N.A.
RF STRAIN-MOSCOW;
RI MEDLINE: 94082441.
RA SENKEVICH T.G., KOONIN E.V., BULLER R.M.;
RT "A poxvirus protein with a RING zinc finger motif is of crucial importance for virulence."
RL Virology 198:118-128(1993).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR EMBL: U01161; AAA16258.1; .
DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
DR PFAM: PF00097; 2f-C3HC4; 1.
KW Zinc-finger.
SQ SEQUENCE 241 AA; 28382 MW; 361D7C30 CRC32;

Query Match 5.9%; Score 6; DB 14; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 NTSSID 14
|||||
Qy 30 NTSSID 35

RESULT 48
ID P87607 PRELIMINARY; PRT; 242 AA.
AC P87607;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE 41KBP FRAGMENT FROM LEFT END OF GENOME.
GN D7R OR C7R.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
RN [1]
RP SEQUENCE FROM N.A.
RF STRAIN-GRI-90;
RI MEDLINE: 97068532.
RA SAFRONOV P.F., PETROV N.A., RIYAZANKINA O.I., TOTMENIN A.V.,
RA SHELKUNOV S.N., SANDAKHCHIEV L.S.;
RT "Genes of a circle of hosts for the cowpox virus."
RL Dokl. Akad. Nauk 349:829-833(1996).
RN [2]
RP SEQUENCE FROM N.A.
RF STRAIN-GRI-90;
RI MEDLINE: 98229462.
RA SHELKUNOV S.N., SAFRONOV P.F., TOTMENIN A.V., PETROV N.A.,
RA RIYAZANKINA O.I., GUTOV V.V., KOTWAL G.J.;
RT "The genomic sequence analysis of the left and right species-specific terminal region of a cowpox virus strain reveals unique sequences and a cluster of intact ORFs for immunomodulatory and host range proteins."
RL Virology 243:432-460(1998).
CC -1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.

DR EMBL: X94355; CAA64092.1; .
DR EMBL: Y11842; CAA72557.1; .
DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
DR PFAM: PF00097; 2f-C3HC4; 1.
KW Zinc-finger.
SQ SEQUENCE 242 AA; 28569 MW; 4BD9333D CRC32;

Query Match 5.9%; Score 6; DB 14; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 NTSSID 14
|||||
Qy 30 NTSSID 35

RESULT 49
ID O80074 PRELIMINARY; PRT; 249 AA.
AC O80074;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE ANTI REPRESSOR.
OS bacteriophage phi PVL.
OC Viruses.
RN [1]
RP SEQUENCE FROM N.A.
RI MEDLINE: 98067870.
RA KANEKO J., KIMURA T., KAWAKAMI Y., TOMITA T., KAMIO Y.;
RT "Panton-valentine leukocidin genes in a phage-like particle isolated from mitomycin C-treated *Staphylococcus aureus* V8 (ATCC 49775).";
RL Biosci. Biotechnol. Biochem. 61:1960-1962(1997).
DR EMBL: AB009866; BAA31909.1; .
SQ SEQUENCE 249 AA; 28536 MW; 057CB5A4 CRC32;

Query Match 5.9%; Score 6; DB 9; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 60 SVLTST 65
|||||
Qy 16 SVLTST 21

RESULT 50
ID O24048 PRELIMINARY; PRT; 253 AA.
AC O24048;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE TONOPLAST INTRINSIC PROTEIN.
GN MBPY OR TIP.
OS Mesembryanthemum crystallinum (Common ice plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllales; Alzooaceae;
OC Mesembryanthemum.
RN [1]
RP SEQUENCE FROM N.A.
RF ISHITANI M., BOHNERT H.J.;
RI Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE MIP FAMILY OF TRANSMEMBRANE CHANNEL PROTEINS.
DR EMBL: U43291; AAB17284.1; .
DR MENDEL; 26903; Meser; mbpy; 26903.
DR PROSITE: PS00221; MIP; 1.
DR PFAM: PF00230; MIP; 1.
DR PRINTS: PR00783; MINTRINSCP.
KW Transport; Transmembrane.
SQ SEQUENCE 253 AA; 26080 MW; 617BA59F CRC32;

Query Match 5.9%; Score 6; DB 10; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 110 QLAGSS 115
|||||
Qy 62 QLAGSS 67

RESULT 51
ID Q62891 PRELIMINARY; PRT; 254 AA.
AC Q62891;
DT 01-JAN-1998 (TREMBLrel. 01, Created)
DT 01-NOV-1998 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE SEC22 HOMOLOG.
GN RSEC22.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-SPRAGUE DAWLEY;
RX MEDLINE; 96215028.
RA HAY J.C., HIRLING H., SCHELLER R.H.;
RT "Mammalian vesicle trafficking proteins of the endoplasmic reticulum
RL J. Biol. Chem. 271:5671-5679(1996).
DR EMBL; U42209; AAB03367.1; -;
DR HSSP; P09012; 201A.
DR PFAM; PF00957; synaptobrevin; 1.
SQ SEQUENCE 254 AA; 28344 MW; E90E9AC4 CRC32;

Query Match 5.9%; Score 6; DB 11; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 133 STKINL 138
|||||
Qy 82 STKINL 87

RESULT 52
ID O18439 PRELIMINARY; PRT; 256 AA.
AC O18439;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE DIVERGED SERINE PROTEASE PRECURSOR.
GN Helicoverpa armigera (Cotton bollworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuoidea; Noctuidae; Heliothinae; Helicoverpa.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-MIDGUT;
RX MEDLINE; 98067794.
RA BOWN D.P., WILKINSON H.S., GATEHOUSE J.A.;
RT "Differentially regulated inhibitor-sensitive and insensitive protease
RT genes from the phytophagous insect pest, Helicoverpa armigera, are
RT members of complex multigene families".
RL Insect Biochem. Mol. Biol. 27:625-638(1997).
DR EMBL; Y12274; CAA72953.1; -;
DR HSSP; P35049; 1TRY.
DR PFAM; PF00089; trypsin; 1.
KW Signal; Protease.
FT SIGNAL 1 21 POTENTIAL.
SQ SEQUENCE 256 AA; 27321 MW; 869C9029 CRC32;

Query Match 5.9%; Score 6; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 51 GSVLTS 56
|||||

Qy 15 GSVLTS 20

RESULT 53
ID O76297 PRELIMINARY; PRT; 257 AA.
AC O76297; O76298; O76299;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE ACCESSORY GLAND-SPECIFIC PEPTIDE 26AA (FRAGMENT).
GN ACP26AA.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-VARIOUS STRAINS;
RX MEDLINE; 98384843.
RA TSAUR S.-C., TING C.-T., WU C.-I.;
RT "Positive selection driving the evolution of a gene of male
RT reproduction, Acp26Aa, of Drosophila: II. Divergence versus
RT polymorphism".
RL Mol. Biol. Evol. 15:1040-1045(1998).
DR EMBL; AF052470; AAC27995.1; -;
DR EMBL; AF052471; AAC27997.1; -;
DR EMBL; AF052472; AAC27999.1; -;
DR EMBL; AF052473; AAC28001.1; -;
DR EMBL; AF052474; AAC28003.1; -;
DR EMBL; AF052475; AAC28005.1; -;
DR EMBL; AF052476; AAC28007.1; -;
DR EMBL; AF052477; AAC28009.1; -;
DR EMBL; AF052478; AAC28011.1; -;
DR EMBL; AF052479; AAC28013.1; -;
DR EMBL; AF052480; AAC28015.1; -;
DR EMBL; AF052481; AAC28017.1; -;
DR EMBL; AF053250; AAC28790.1; -;
DR EMBL; AF053251; AAC28792.1; -;
DR EMBL; AF053252; AAC28794.1; -;
DR EMBL; AF053253; AAC28796.1; -;
DR EMBL; AF053254; AAC28798.1; -;
DR EMBL; AF053255; AAC28800.1; -;
DR EMBL; AF053256; AAC28802.1; -;
DR EMBL; AF053257; AAC28804.1; -;
DR EMBL; AF053258; AAC28806.1; -;
DR EMBL; AF053259; AAC28808.1; -;
DR EMBL; AF053260; AAC28810.1; -;
DR EMBL; AF053261; AAC28812.1; -;
DR EMBL; AF053262; AAC28814.1; -;
DR EMBL; AF053263; AAC28816.1; -;
DR EMBL; AF053264; AAC28818.1; -;
DR EMBL; AF053265; AAC28820.1; -;
DR EMBL; AF053266; AAC28822.1; -;
DR EMBL; AF053267; AAC28824.1; -;
DR EMBL; AF053268; AAC28826.1; -;
DR EMBL; AF053269; AAC28828.1; -;
DR EMBL; AF053270; AAC28830.1; -;
DR EMBL; AF053271; AAC28832.1; -;
DR EMBL; AF053272; AAC28834.1; -;
DR EMBL; AF053273; AAC28836.1; -;
DR EMBL; AF053274; AAC28838.1; -;
DR EMBL; AF053275; AAC28840.1; -;
DR EMBL; AF053276; AAC28842.1; -;
KW Glycoprotein; Behavior; Polymorphism.
FT NON_TER 1 1
FT VARIANT 12 12 N -> S (IN STRAINS AF2, AF3, AF5, AF7,
AF10, AU2, AU4, AU5, AU6, AU8, AU10, NY2,
NY3, NY4, NY5, NY7, TW1, TW4, TW5, TW7,
TW8 AND TW11)
FT VARIANT 18 18 Q -> K (IN STRAINS AU6, NY1, NY2, NY6,
NY8, TW2, TW3, TW4, TW7, TW9 AND TW10).
FT VARIANT 25 25 L -> Q (IN STRAINS AF2, AF7, AU4, NY3,
NY5 AND TW11).
FT FT

FT VARIANT 32 32 S -> G (IN STRAIN NY2).

FT VARIANT 33 33 A -> S (IN STRAIN AU3).

FT VARIANT 37 39 NVP -> SVT (IN STRAIN AU3).

FT VARIANT 39 39 P -> T (IN STRAINS AF2, AF7, AU5, AU9, NY3, NY5, NY7, TW10 AND TW11).

FT VARIANT 49 49 I -> L (IN STRAIN AU3).

FT VARIANT 58 58 D -> G (IN STRAIN AF6).

FT VARIANT 72 72 D -> N (IN STRAINS AU2, AU3, AU8, NY4, TW1, TW5 AND TW8).

FT VARIANT 94 94 N -> S (IN STRAINS AF1, AF2, AF3, AF5, AF6, AF7, AF8, AF9, AF10, AU3, AU4, AU6, AU7, NY2, NY3, NY5, NY6, TW3, TW4, TW6, TW7, TW10 AND TW11).

FT VARIANT 102 102 L -> I (IN STRAINS AF1, AF2, AF3, AF5, AF6, AF7, AF8, AF9, AF10, AU2, AU4, AU6, AU7, AU8, NY2, NY3, NY4, NY5, TW1, TW3, TW4, TW5, TW6, TW7, TW8, TW10 AND TW11).

FT VARIANT 165 165 E -> Q (IN STRAINS AU1, AU3 AND AU9).

FT VARIANT 200 200 S -> I (IN STRAINS AU5 AND NY2).

FT VARIANT 205 205 A -> V (IN STRAIN NY2).

FT VARIANT 214 214 R -> K (IN STRAIN TW2).

FT VARIANT 219 219 N -> Y (IN STRAIN TW9).

FT VARIANT 246 246 E -> D (IN STRAINS AF6, AF8, AF9, AU4, TW1 AND TW11).

FT VARIANT 255 255 P -> S (IN STRAINS AF5, AF10, AU5 AND TW10).

FT SEQUENCE 257 AA; 28855 MW; 92837F1D CRC32;

Query Match 5.9%; Score 6; DB 5; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 89 SSIDLN 94
QY 32 SSIDLN 37

RESULT 54
ID P96891 PRELIMINARY; PRT; 261 AA.
AC P96891;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE SIGF.
DE SIGF.
GN SIGF.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
RN [1]
RA STRAIN-H37RV;
RA OLIVER K., HARRIS D.;
RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RC STRAIN-H37RV;
RC STRAIN-H37RV;
RC BARRELL B.G., RAJANDREAM M.A.;
RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RC STRAIN-H37RV;
RC MEDLINE; 96181548.
RX PHILLIP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
RA COLE S.T.;
RA "An integrated map of the genome of the tubercle bacillus,
Mycobacterium tuberculosis H37RV, and comparison with Mycobacterium leprae."
RL Proc. Natl. Acad. Sci. U.S.A. 93:3132-3137(1996).
DR EMBL; 292771; CAB07069.1; -;
DR PFAM; PF00140; sigma70; 1.
SQ SEQUENCE 261 AA; 28793 MW; EBF9A006 CRC32;

Query Match 5.9%; Score 6; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 145 SELAAE 150
QY 67 SELAAE 72

RESULT 55
ID Q50547 PRELIMINARY; PRT; 261 AA.
AC Q50547;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE STRESS RESPONSE/STATIONARY PHASE SIGMA FACTOR.
GN SIGF.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
RN [1]
RA SEQUENCE FROM N.A.
RA STRAIN-H37RV;
RA MEDLINE; 96181544.
RA DEMAYO J., ZHANG Y., KO C., YOUNG D.B., BISHAI W.R.;
RA "A stationary-phase stress-response sigma factor from Mycobacterium tuberculosis."
RL Proc. Natl. Acad. Sci. U.S.A. 93:2790-2794(1996).
DR EMBL; U41061; AAC44103.1; -;
DR PFAM; PF00140; sigma70; 1.
SQ SEQUENCE 261 AA; 28779 MW; 5F7C46F1 CRC32;

Query Match 5.9%; Score 6; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 145 SELAAE 150
QY 67 SELAAE 72

RESULT 56
ID Q92EP8 PRELIMINARY; PRT; 266 AA.
AC Q92EP8;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE 3-METHYL-2-OXOBUTANOATE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.11).
GN PANB.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
OC Pseudomonas.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SBW25;
RA RAINNEY P.B.;
RA "Adaptation of Pseudomonas fluorescens to the plant rhizosphere."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SBW25;
RX MEDLINE; 96228701.
RA RAINNEY P.B., BAILEY M.J.;
RA "Physical and genetic map of the Pseudomonas fluorescens SBW25 chromosome";
RL Mol. Microbiol. 19:521-533(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-SBW25;
RX MEDLINE; 98000889.
RA RAINNEY P.B., HEITHOFF D.M., MAHAN M.J.;
RA "Single-step conjugative cloning of bacterial gene fusions involved in
microbe-host interactions.";

RL Mol. Gen. Genet. 256:84-87(1997).
 DR EMBL; AJ130846; CAA10222.1; -.
 KW Transferase; Methyltransferase.
 SQ SEQUENCE 266 AA; 27969 MW; C3017E41 CRC32;

Query Match 5.9%; Score 6; DB 2; Length 266;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 185 SELAAE 190

QY 67 SELAAE 72

RESULT 57
 ID Q52256 PRELIMINARY; PRT; 274 AA.

AC Q52256;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE N-ACETYLIMANNOSAMINE TRANSFERASE.
 GN RFBA.

OS Salmonella borreze.
 OG Plasmid pMQ799.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 95394842.

RA KEENEYSIDE W.J.; WHITFIELD C.;

RT "Lateral transfer of rfb genes: a mobilizable ColeI-type plasmid carries the rfbO:54 (O:54 antigen biosynthesis) gene cluster from
 RT Salmonella enterica serovar Borreze.";
 RL J. Bacteriol. 177:5247-5253(1995).

DR EMBL; L39794; AAC98401.1; -.

KW Transferase; Plasmid.

SQ SEQUENCE 274 AA; 31799 MW; BA21AE0D CRC32;

Query Match 5.9%; Score 6; DB 2; Length 274;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 170 GGYNTS 175

QY 27 GGYNTS 32

RESULT 58
 ID Q51718 PRELIMINARY; PRT; 278 AA.

AC Q51718;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE PHA DEPOLYMERASE PRECURSOR.
 GN PHAZ.

OS Pseudomonas fluorescens.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
 OC Pseudomonas.
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-DSM 7139;

RX MEDLINE; 95050280.

RA SCHIRMER A.; JENDROSSEK D.;

RT "Molecular characterization of the extracellular poly(3-hydroxyoctanoic acid) [P(3HO)] depolymerase gene of Pseudomonas fluorescens GK13 and of its gene product.";
 RT J. Bacteriol. 176:7065-7073(1994).
 DR EMBL; U10470; AAA64538.1; -.

KW Signal.

FT SIGNAL.

FT CHAIN

SQ SEQUENCE 278 AA; 30267 MW; 2C97E460 CRC32;

Query Match 5.9%; Score 6; DB 2; Length 278;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 174 GGYNTS 179

QY 27 GGYNTS 32

RESULT 59

ID O65061 PRELIMINARY; PRT; 281 AA.

AC O65061;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DE ATAF1-LIKE PROTEIN (FRAGMENT).

GN SB29.

OS Picea mariana (Black spruce).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC ephylliphytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;

OC Picea.

RN [1]

RP SEQUENCE FROM N.A.

RA PERRY D.J.; BOUSQUET J.;

RL Genetics 0:0-0(1998).

DR EMBL; AF051222; AAC32123.1; -.

DR MENDEL; 28845; Picma; 3421; 28845.

FT NON_TER

SQ SEQUENCE 281 AA; 31510 MW; 0B06B236 CRC32;

Db 139 TCYN5A 144

QY 7 TCYN5A 12

Query Match 5.9%; Score 6; DB 10; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 139 TCYN5A 144

QY 7 TCYN5A 12

RESULT 60
 ID Q9Y682 PRELIMINARY; PRT; 282 AA.

AC Q9Y682;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DE SEC22 HOMOLOG.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RA ZHOU J.; YE M.; FU G.; ZHANG Q.; GUAN Z.; HUANG Q.; XU S.; GU B.;

RA CHEN S.; SHEN Y.; CHEN Z.;

RT "Human Sec 22 homolog gene.";

RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF100749; AAD43013.1; -.

SQ SEQUENCE 282 AA; 31719 MW; EC2FAC69 CRC32;

Db 133 STKINL 138

QY 82 STKINL 87

RESULT 61

ID O23186 PRELIMINARY; PRT; 284 AA.

AC O23186;

DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DE HEAT SHOCK TRANSCRIPTION FACTOR HSF4.
GN HSF4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eukaryotes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RA BEVAN M., TERRYN N., VOS P., HEIJNEN L., MEWES H.W., SCHUELLER C.,
RA CHALWATZIS N.:
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU ARABIDOPSIS SEQUENCING PROJECT ESSA;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-GREEN SILIQUES;
RX MEDLINE; 98307340.
RA PRAENDL R., HINDERHOFER K., EGGERS-SCHUMACHER G., SCHOEFL F.;
"HSF3, a new heat shock factor from Arabidopsis thaliana, derepresses
the heat shock response and confers thermotolerance when overexpressed
in transgenic plants.";
RL MOL. Gen. Genet. 258:269-278(1998).
DR EMBL; Z99707; CAB16764.1; -.
DR EMBL; Y14069; CAA74398.1; -.
DR HSP; P22813; IHKS.
DR MENDEL; 25505; Arath;1416;25505.
DR PFAM; PF00447; HSF_DNA-bind; 1.
DR PRINTS; PR00056; HSFDOMAIN.
KW Heat shock.
SQ SEQUENCE 284 AA; 31328 MW; 206AB5DC CRC32;

Query Match 5.9%; Score 6; DB 10; Length 284;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 171 SSELAA 176
QY 66 SSELAA 71
|||||

RESULT 62
ID Q96320 PRELIMINARY; PRT; 284 AA.
AC Q96320;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE HEAT SHOCK TRANSCRIPTION FACTOR.
GN HSF4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eukaryotes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-COLUMBIA; TISSUE=LEAVES, AND STEM;
RA NOVER L., SCHARF K., GAGLIARDI D., VERGNE P., CZARNECKA-VERNER E.,
RA GURLEY W.;
RL Cell Stress and Chaperones 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA; TISSUE=LEAVES, AND STEM;
RA BARROS D., CZARNECKA-VERNER E., YUAN C.X., BALDWIN D., GURLEY W.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U68017; AAC31756.1; -.
DR HSP; P22813; IHKS.
DR MENDEL; 7027; Arath;1416;7027.
DR PFAM; PF00447; HSF_DNA-bind; 1.
DR PRINTS; PR00056; HSFDOMAIN.
KW Heat shock.

SQ SEQUENCE 284 AA; 31397 MW; 2F6634C0 CRC32;

Query Match 5.9%; Score 6; DB 10; Length 284;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 171 SSELAA 176
QY 66 SSELAA 71
|||||

RESULT 63
ID O28681 PRELIMINARY; PRT; 286 AA.
AC O28681;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE HYPOTHETICAL 31.5 KD PROTEIN.
GN AF1591.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE; 98049343.
RA KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
RA KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RA RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRIDES N.C.,
RA FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
RA PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
RA OVERBEK R., GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T.,
RA COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,
RA SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
RA VENTER J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
DR EMBL; AF000992; AAB89657.1; -.
DR TIGR; AF1591; -.
DR PFAM; PF01402; HTH_4; 1.
KW Hypothetical protein.
SQ SEQUENCE 286 AA; 31519 MW; ACE53FAD CRC32;

Query Match 5.9%; Score 6; DB 1; Length 286;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 125 LTSTCE 130
QY 18 LTSTCE 23
|||||

RESULT 64
ID O87560 PRELIMINARY; PRT; 294 AA.
AC O87560;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE HYPOTHETICAL 32.8 KD PROTEIN.
GN
OS Bacillus firmus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OF4;
RA WEI Y., GUFFANTI A.A., KRULWICH T.A.;
RT "Sequence analysis and functional studies of a chromosomal region of
alkaliphilic Bacillus firmus OF4 encoding an ABC-type transporter with
similarity of sequence and Na⁺ exclusion capacity to the Bacillus
RT subtilis Natab transporter.";

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF084104; AAC62419.1; -.
 DR PFAM; PF00592; DUF3; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 294 AA; 32773 MW; 85FE92D3 CRC32;

Query Match 5.9%; Score 6; DB 2; Length 294;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 22 NIDGTL 27

Qy 93 NIDGTL 98

RESULT 65
 ID Q98251 PRELIMINARY; PRT; 298 AA.
 AC Q98251;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE MC084L.
 GN MC084L.
 OS Molluscum contagiosum virus subtype 1 (MCV1), and
 OS Molluscum contagiosum virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Molluscipoxvirus.
 RN [1]
 RN SEQUENCE FROM N.A.
 RP RP
 RX MEDLINE; 96325459.
 RA SENKEVICH T.G., BUGERT J.J., SISLER J.R., KOONIN E.V., DARAI G.,
 RA MOSS B.;
 RT "Genome sequence of a human tumorigenic poxvirus: prediction of
 RT specific host response-evasion genes.";
 RL Science 273:813-816(1996).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP RP
 RA SENKEVICH T.G., BUGERT J.J., SISLER J.R., KOONIN E.V., DARAI G.,
 RA MOSS B.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RP RP
 RC STRAIN-SUBTYPE 1-VARIANT;
 RX MEDLINE; 98125989.
 RA WATANABE T., MORIKAWA S., SUZUKI K., MIYAMURA T., TAMAKI K., UEDA Y.;
 RT "Two major antigenic polypeptides of molluscum contagiosum virus.";
 RL J. Infect. Dis. 177:284-292(1998).
 RN [4]
 RN EMBL; U60315; AAC55212.1; -.
 RN EMBL; AB004838; BAA25418.1; -.
 SQ SEQUENCE 298 AA; 32040 MW; 1561F2FD CRC32;

Query Match 5.9%; Score 6; DB 14; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 203 LAGSSE 208

Qy 63 LAGSSE 68

RESULT 66
 ID Q9Y3Q9 PRELIMINARY; PRT; 306 AA.
 AC Q9Y3Q9;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE ECTO-ATP DIPHOSPHOHYDROLASE II (EC 3.6.1.5).
 GN PLEA 2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RN SEQUENCE FROM N.A.

RC TISSUE-PLACENTA;
 RA MATSUMOTO M., SAKURAI Y., KOKUBO T., YAGI H., MATSUI T., TITANI K.,
 RA FUJIMURA Y., NARITA N.;
 RT "The cDNA cloning of human placental ecto-ATP diphosphohydrolases I
 RT and II.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ133134; CAB41887.1; -.
 DR PROSITE; PS01238; GDAL_CD39_NTPASE; 1.
 KW Hydrolase.
 SQ SEQUENCE 306 AA; 34175 MW; 2F33C431 CRC32;

Query Match 5.9%; Score 6; DB 4; Length 306;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 193 LGKFSQ 198

Qy 1 LGKFSQ 6

RESULT 67
 ID O60987 PRELIMINARY; PRT; 311 AA.
 AC O60987;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE G2-LIKE.
 GN G2.
 OS Dictyostelium discoideum (Slime mold).
 OC Plasmid Ddp5.
 OC Eukaryota; Dictyosteliida; Dictyostelium.
 RN [1]
 RN SEQUENCE FROM N.A.
 RP RP
 RC STRAIN-WS2162;
 RX MEDLINE; 98198836.
 RA RIEBEN W.K. JR., GONZALES C.M., GONZALES S.T., PILKINGTON K.J.,
 RA KIYOSAWA H., HUGHES J.E., WELKER D.L.;
 RT "Dictyostelium discoideum nuclear plasmid ddp5 is a chimera related to
 RT the Ddp1 and Ddp2 plasmid families.";
 RL Genetics 148:1117-1125(1998).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP RP
 RC STRAIN-WS2162;
 RA RIEBEN W.K., GONZALES C., GONZALES S.T., PILKINGTON K., KIYOSAWA H.,
 RA HUGHES J.E., WELKER D.L.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF000580; AAC14394.1; -.
 KW Plasmid.
 SQ SEQUENCE 311 AA; 36889 MW; 2D354975 CRC32;

Query Match 5.9%; Score 6; DB 5; Length 311;
 Best Local Similarity 100.0%; Pred. No. 1.80e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 110 VSTKIN 115

Qy 81 VSTKIN 86

RESULT 68
 ID O14047 PRELIMINARY; PRT; 312 AA.
 AC O14047;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE HYPOTHEICAL 35.2 KD PROTEIN C2C4.14C IN CHROMOSOME I.
 GN SPAC2C4.14C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Archiascomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 RN [1]
 RN SEQUENCE FROM N.A.

RC STRAIN-972;
RA OLIVER K., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WOOD V.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
PROTEIN KINASES. STRONGEST TO THE STE20 SUBFAMILY.
DR EMBL; 299259; CAB16374.1; -;
DR PFAM; PF00069; pkinase; 1;
KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW ATP-binding.
FT BINDING 35 35 ATP (BY SIMILARITY).
FT ACT_SITE 127 127 BY SIMILARITY.
SQ SEQUENCE 312 AA: 35218 MW; 7576E17B CRC32;

Query Match 5.9%; Score 6; DB 3; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 57 IDLSNV 62
| | | | |
QY 34 IDLSNV 39
| | | | |
RC BLT 69
ID C08964 PRELIMINARY; PRT; 313 AA.
AC C08964;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DE 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE PROTOCOLADHERIN 5 (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RA OBATA S., SAGO H., MORI N., DAVIDSON M., ST JOHN T., SHINTARO S.T.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB004277; BAA20360.1; -;
FT NON_TER 1 1
SQ SEQUENCE 313 AA: 33922 MW; F2F03E66 CRC32;

Query Match 5.9%; Score 6; DB 11; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 123 DGLTKY 128
| | | | |
QY 95 DGLTKY 100
| | | | |
RC T 70
ID Q12145 PRELIMINARY; PRT; 317 AA.
AC Q12145;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE HYPOTHETICAL 35.4 KD PROTEIN IPR012C.
GN IPR012C OR LPZ12C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AB972;
RA BADCOCK K., BOWMAN S., CHURCHER C.M., PEARSON D., RAJANDREAM M.A.,
RA WALSH S.V., BARRELL B.G.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-AB972;
RA BOWMAN S.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

RC STRAIN-AB972;
RA BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA WANG Y., AHMED A., BUSSEY H., FORTIN N., FRIESEN J.D., HALL J.,
RA STORMS R.K., VO D.H., WINNETT E.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86028187.
RA HIEFER P., PRIDMORE D., HEGEMANN J.H., THOMAS M., DAVIS R.W.,
RA PHILIPPSEN P.;
RT "Functional selection and analysis of yeast centromeric DNA.";
RL Cell 42:913-921(1985).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91117242.
RA YANO R., NOMURA M.;
RT "Suppressor analysis of temperature-sensitive mutations of the largest
subunit of RNA polymerase I in Saccharomyces cerevisiae: a suppressor
gene encodes the second-largest subunit of RNA polymerase I.";
RL Mol. Cell. Biol. 11:754-764(1991).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92371421.
RA GAXIOLA R., DE LARRINOA I.F., VILLALBA J.M., SERRANO R.;
RT "A novel and conserved salt-induced protein is an important
determinant of salt tolerance in yeast.";
RL EMBO J. 11:3157-3164(1992).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93156813.
RA MOYA M., ROBERTS D., NOVICK P.;
RT "DSS4-1 is a dominant suppressor of sec4-8 that encodes a nucleotide
exchange protein that aids Sec4p function.";
RL Nature 361:460-463(1993).
DR EMBL; Z71255; CAA95009.1; -;
DR EMBL; Z49919; CAA90157.1; -;
DR EMBL; U31900; AAA97591.1; -;
DR PROSITE; PS00028; ZINC_FINGER_C2H2; 2.
DR PFAM; PF00096; zf-C2H2; 2.
DR PRINTS; PR00048; ZINC_FINGER.
KW Hypothetical protein; Zinc-finger; Metal-binding; DNA-binding.
SQ SEQUENCE 317 AA; 35358 MW; 5E32D6BE CRC32;

Query Match 5.9%; Score 6; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.80e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 69 STKINL 74
| | | | |
QY 82 STKINL 87
| | | | |
RESULT 71
ID QY028 PRELIMINARY; PRT; 324 AA.
AC QY028;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE GAG-RELATED PROTEIN (FRAGMENT).
GN ORF3.
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TULAHUEN;
RX MEDLINE; 95205412.
RA MARTIN F., MARANON C., OLIVARES M., ALONSO C., LOPEZ M.C.;
RT "Characterization of a non-long terminal repeat retrotransposon cDNA
(Litc) from Trypanosoma cruzi; homology of the first ORF with the ape
family of DNA repair enzymes.";


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RL J. Mol. Biol. 247:49-59(1995).
DR EMBL; X83098; CAB41694.1; -.
FT NON_TER 1
SQ SEQUENCE 324 AA; 36941 MW; DE1604F2 CRC32;

Query Match
Best Local Similarity 100.0%; Score 6; DB 5; Length 324;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 294 LGKFSQ 299
    |||||
QY 1 LGKFSQ 6

RESULT 72
ID O07641 PRELIMINARY; PRT; 327 AA.
AC O07641
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
LN NITROGENASE REDUCTASE.
GN NIFH.
OS Cyanothecae (strain ATCC 51142).
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC51142;
RA COLON-LOPEZ M., SHERMAN L.A.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003336; AAB61408.1; -.
DR HSP; P00459; INIP.
DR PROSITE; PS00692; NIFH_FRXC_2; 1.
DR PROSITE; PS00746; NIFH_FRXC_1; 1.
DR PFAM; PF00142; fer4_NifH; 1.
DR PRINTS; PR00091; NITROGNASEII.
SQ SEQUENCE 327 AA; 35822 MW; F3315D74 CRC32;

Query Match
Best Local Similarity 100.0%; Score 6; DB 2; Length 327;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 22 QPSNFI 27
    |||||
QY 50 QPSNFI 55

RESULT 73
ID Q09026 PRELIMINARY; PRT; 337 AA.
AC Q09026
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE PLASMID RECOMBINATION ENZYME (MOBILIZATION PROTEIN).
GN MOB13.
OS Enterococcus oeni (Leuconostoc oenos).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
OC Enterococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-8413;
RX MEDLINE; 94134826.
RA FREMAUX C., AIGLE M., LONVAUD-FUNEL A.;
RT "Sequence analysis of Leuconostoc oenos DNA: organization of pLO13, a
cryptic plasmid."
RL Plasmid 30:212-223(1993).
CC -!- FUNCTION: THE INTERACTION OF THE RSA SITE AND THE PRE PROTEIN MAY
NOT ONLY SERVES A FUNCTION IN PLASMID MAINTENANCE, BUT ALSO MAY
CONTRIBUTES TO THE DISTRIBUTION OF SMALL ANTIBIOTIC RESISTANCE
PLASMIDS AMONG GRAM-POSITIVE BACTERIA.
CC -!- MISCELLANEOUS: PRE PROTEINS CONTAIN CONSERVED POSITIVELY CHARGED
AMINO ACIDS PROBABLY INVOLVED IN THE BINDING OF THE PRE PROTEIN TO
THE RSA SITE.

CC -!- SIMILARITY: TO OTHER PRE PROTEINS (FROM PLASMIDS PUB110, PMV158,
PE194, PT181, PTB913), IN THEIR N-TERMINAL ONLY.
DR EMBL; M95954; AAA19673.1; -.
DR PFAM; PF01076; Mob_Pre; 1.
KW Plasmid; DNA-binding.
FT BINDING 113 113 DNA (BY SIMILARITY).
SQ SEQUENCE 337 AA; 39863 MW; DIC982CE CRC32;

Query Match
Best Local Similarity 100.0%; Score 6; DB 2; Length 337;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 233 KINLDD 238
    |||||
QY 84 KINLDD 89

RESULT 74
ID O77146 PRELIMINARY; PRT; 339 AA.
AC O77146
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE SJRI (FRAGMENT).
GN RT.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CHINESE; TISSUE-MIRACIDIUM;
RA FAN J., BRINDLEY P.J.;
RT "Retrotransposable elements in the Schistosoma japonicum genome.";
RL (In) Tada I., Kojima S., Tsuji M. (eds.);
RL Proceedings of the 9th international congress of parasitology (ICOPA
IX), pp.821-825, Monduzzi Editore, Bologna (1998).
DR EMBL; AF073333; AAC62955.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1
SQ SEQUENCE 339 AA; 39335 MW; 22B00C22 CRC32;

Query Match
Best Local Similarity 100.0%; Score 6; DB 5; Length 339;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 60 IQGSVL 65
    |||||
QY 13 IQGSVL 18

RESULT 75
ID O9YWP5 PRELIMINARY; PRT; 347 AA.
AC O9YWP5
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE VP7.
OS Coltivirus JKT-7075.
OC Viruses; dsRNA viruses; Reoviridae; Coltivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JKT-7075;
RX MEDLINE; 98451335.
RA ATTOUTI H., CHARREL R.N., BILLOIR F., CANTALOUBE J.F., DE MICCO P.,
RA DE LAMBALLERIE X.;
RT "Comparative sequence analysis of American, European and Asian
isolates of viruses in the genus Coltivirus.";
RL J. Gen. Virol. 79:0-0(0).
DR EMBL; AF052023; AAC72050.1; -.
SQ SEQUENCE 347 AA; 38942 MW; 957291C6 CRC32;

Query Match
Best Local Similarity 100.0%; Score 6; DB 14; Length 347;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 79 IDLNSV 84

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Qy 34 IDLNSV 39

Search completed: Wed Aug 16 09:57:02 2000
Job time : 54 secs.